85933

STIC-Biotech/Ch mLib

12E18

From: Schultz, James
Sent: Tuesday, February 04, 2003 10:18 AM
To: STIC-Biotech/ChemLib
Subject: Sequence search 09/960,143

Hello,
Could you please run a length limited nucleotide sequence search on SEQ ID NO:3 (1639 nt long) in the above entitled application, where the maximum size of the returned hits are no longer than 50 nucleotides?
Thanks,
Doug Schultz

J. Douglas Schultz, Ph.D.
AU 1635 (Biotechnology)
Patent Examiner
United States Patent and Trademark Office
(703) 308-9355
(703) 746-3973 (fax)
Office: CM1 12E18
Mail: CM1 11E12

CRF

Point of Contact:
Thomas G. Larson, Ph.D.
703-308-7309
CM1, Rm. 6 B 01

Searcher: Larson
Phone:
Location:
Date Picked Up: 2/4
Date Completed: 2/13
Searcher Prep/Review: 10
Clerical:
Online time: 5

TYPE OF SEARCH:
NA Sequences: 1
AA Sequences:
Structures:
Bibliographic:
Litigation:
Full text:
Patent Family:
Other:

VENDOR/COST (where applic.)
STN:
DIALOG:
Questel/Orbit:
DRLink:
Lexis/Nexis:
Sequence Sys.: ABSS03
WWW/Internet:
Other (specify):

GenCore version 5.1.3

OM nucleic - nucleic search, using sw model

Run on: February 9, 2003, 17:22:03 ; Search time 101 Seconds
(without alignments)
4976.665 Million cell updates/sec

Title: US-09-960-143-3
Perfect score: 1639
Sequence: 1 acaaactttcagagacagca.....atataatttgttgtcaaagt 1639

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 609818

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
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2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	37.4	2.3	47	1	US-08-330-163-42	Sequence 42, Appl
	2	37.4	2.3	47	1	US-08-482-111-42	Sequence 42, Appl
c	3	37	2.3	37	1	US-08-330-163-40	Sequence 40, Appl
c	4	37	2.3	37	1	US-08-482-111-40	Sequence 40, Appl
c	5	33	2.0	33	2	US-08-410-654B-42	Sequence 42, Appl
c	6	33	2.0	33	2	US-08-474-851-42	Sequence 42, Appl
c	7	33	2.0	33	2	US-08-481-560-42	Sequence 42, Appl
c	8	31	1.9	31	5	PCT-US96-08142-9	Sequence 9, Appli
c	9	30	1.8	30	4	US-09-308-160B-6	Sequence 6, Appli
c	10	30	1.8	30	4	US-09-456-399-6	Sequence 6, Appli
	11	28	1.7	28	2	US-08-859-998-479	Sequence 479, App
c	12	28	1.7	28	2	US-08-859-998-480	Sequence 480, App
	13	28	1.7	28	4	US-09-225-928-479	Sequence 479, App
c	14	28	1.7	28	4	US-09-225-928-480	Sequence 480, App
c	15	25	1.5	25	1	US-08-327-494A-8	Sequence 8, Appli
c	16	25	1.5	25	5	PCT-US95-13659-8	Sequence 8, Appli
c	17	25	1.5	25	5	PCT-US96-08142-8	Sequence 8, Appli
c	18	24	1.5	24	4	US-09-710-200-72	Sequence 72, Appl
	19	24	1.5	24	5	PCT-US96-08142-7	Sequence 7, Appli
c	20	23.4	1.4	47	4	US-09-641-638-1167	Sequence 1167, Ap
	21	23	1.4	23	1	US-08-327-494A-7	Sequence 7, Appli
	22	23	1.4	23	5	PCT-US95-13659-7	Sequence 7, Appli
	23	23	1.4	40	1	US-08-482-111-53	Sequence 53, Appl
	24	22	1.3	22	4	US-09-046-894-20	Sequence 20, Appl
	25	22	1.3	48	1	US-08-317-102-1	Sequence 1, Appli
c	26	21.8	1.3	47	4	US-09-338-907-250	Sequence 250, App
c	27	21.8	1.3	47	4	US-09-338-907-327	Sequence 327, App
c	28	21.8	1.3	47	4	US-09-218-207-250	Sequence 250, App
c	29	21.8	1.3	47	4	US-09-218-207-327	Sequence 327, App
c	30	21.8	1.3	48	1	US-08-317-102-2	Sequence 2, Appli
	31	21.6	1.3	41	4	US-09-297-053-20	Sequence 20, Appl
	32	21.6	1.3	47	4	US-09-641-638-1043	Sequence 1043, Ap
c	33	21	1.3	21	1	US-08-246-855A-16	Sequence 16, Appl
	34	21	1.3	21	2	US-08-410-654B-29	Sequence 29, Appl
	35	21	1.3	21	2	US-08-410-654B-41	Sequence 41, Appl
	36	21	1.3	21	2	US-08-474-851-29	Sequence 29, Appl
	37	21	1.3	21	2	US-08-474-851-41	Sequence 41, Appl
	38	21	1.3	21	2	US-08-481-560-29	Sequence 29, Appl
	39	21	1.3	21	2	US-08-481-560-41	Sequence 41, Appl
c	40	21	1.3	21	2	US-08-468-819-28	Sequence 28, Appl
c	41	21	1.3	21	2	US-08-468-819-43	Sequence 43, Appl
	42	21	1.3	21	3	US-08-621-841-15	Sequence 15, Appl
c	43	21	1.3	21	5	PCT-US95-06356-16	Sequence 16, Appl
c	44	21	1.3	45	4	US-09-813-872-14	Sequence 14, Appl
	45	21	1.3	47	4	US-09-641-638-1031	Sequence 1031, Ap

ALIGNMENTS

RESULT 1
US-08-330-163-42
; Sequence 42, Application US/08330163
; Patent No. 5656724
; GENERAL INFORMATION:
; APPLICANT: Daly, Thomas J.
; APPLICANT: LaRosa, Gregory J.
; TITLE OF INVENTION: Chemokine-Like Proteins and Methods of
; TITLE OF INVENTION: Use
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30B
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/330,163
; FILING DATE: 05-AUG-1994
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Fasse, J. Peter
; REGISTRATION NUMBER: 32,983
; REFERENCE/DOCKET NUMBER: 00231/080001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; INFORMATION FOR SEQ ID NO: 42:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 47 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-330-163-42

Query Match 2.3%; Score 37.4; DB 1; Length 47;
Best Local Similarity 87.2%; Pred. No. 15;
Matches 41; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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Qy     169 AGGAGTGCTAAAGAACTTAGATGTCAGTGCATAAAGACATACTCCAA 215
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Db       1 ATGAGTGCTAAAGACCTGCAGTGTCAGTGCATAAAGACATACTCCAA 47
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RESULT 2
US-08-482-111-42
; Sequence 42, Application US/08482111
; Patent No. 5789539
;  GENERAL INFORMATION:
;    APPLICANT:  Daly, Thomas J.
;    APPLICANT:  LaRosa, Gregory J.
;    TITLE OF INVENTION:  Chemokine-Like Proteins and Methods of
;    TITLE OF INVENTION:  Use
;    NUMBER OF SEQUENCES:  70
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fish & Richardson P.C.
;      STREET:  225 Franklin Street
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  U.S.A.
;      ZIP:  02110-2804
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30B
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/482,111
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Fasse, J. Peter
;      REGISTRATION NUMBER:  32,983
;      REFERENCE/DOCKET NUMBER:  00231/083001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 542-5070
;      TELEFAX:  (617) 542-8906
;  INFORMATION FOR SEQ ID NO:  42:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  47 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA
US-08-482-111-42

  Query Match             2.3%;  Score 37.4;  DB 1;  Length 47;
  Best Local Similarity   87.2%;  Pred. No. 15;
  Matches   41;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

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Db       1 ATGAGTGCTAAAGACCTGCAGTGTCAGTGCATAAAGACATACTCCAA 47


RESULT 3
US-08-330-163-40/c
; Sequence 40, Application US/08330163
; Patent No. 5656724
; GENERAL INFORMATION:
;    APPLICANT:  Daly, Thomas J.
;    APPLICANT:  LaRosa, Gregory J.
;    TITLE OF INVENTION:  Chemokine-Like Proteins and Methods of
;    TITLE OF INVENTION:  Use
;    NUMBER OF SEQUENCES:  46
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fish & Richardson
;      STREET:  225 Franklin Street
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  U.S.A.
;      ZIP:  02110-2804
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30B
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/330,163
;      FILING DATE:  05-AUG-1994
;      CLASSIFICATION:  530
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Fasse, J. Peter
;      REGISTRATION NUMBER:  32,983
;      REFERENCE/DOCKET NUMBER:  00231/080001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 542-5070
;      TELEFAX:  (617) 542-8906
;  INFORMATION FOR SEQ ID NO:  40:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  37 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA
US-08-330-163-40

  Query Match             2.3%;  Score 37;  DB 1;  Length 37;
  Best Local Similarity   100.0%;  Pred. No. 18;
  Matches   37;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     351 GGTTGTGGAGAAGTTTTTGAAGAGGGCTGAGAATTCA 387
           |||||||||||||||||||||||||||||||||||||
Db      37 GGTTGTGGAGAAGTTTTTGAAGAGGGCTGAGAATTCA 1


RESULT 4
US-08-482-111-40/c
; Sequence 40, Application US/08482111
; Patent No. 5789539
; GENERAL INFORMATION:
;    APPLICANT:  Daly, Thomas J.
;    APPLICANT:  LaRosa, Gregory J.
;    TITLE OF INVENTION:  Chemokine-Like Proteins and Methods of
;    TITLE OF INVENTION:  Use
;    NUMBER OF SEQUENCES:  70
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fish & Richardson P.C.
;      STREET:  225 Franklin Street
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  U.S.A.
;      ZIP:  02110-2804
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30B
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/482,111
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Fasse, J. Peter
;      REGISTRATION NUMBER:  32,983
;      REFERENCE/DOCKET NUMBER:  00231/083001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 542-5070
;      TELEFAX:  (617) 542-8906
;  INFORMATION FOR SEQ ID NO:  40:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  37 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA
US-08-482-111-40

  Query Match             2.3%;  Score 37;  DB 1;  Length 37;
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  Best Local Similarity   100.0%;  Pred. No. 18;
  Matches   37;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     351 GGTTGTGGAGAAGTTTTTGAAGAGGGCTGAGAATTCA 387
           |||||||||||||||||||||||||||||||||||||
Db      37 GGTTGTGGAGAAGTTTTTGAAGAGGGCTGAGAATTCA 1


RESULT 5
US-08-410-654B-42/c
; Sequence 42, Application US/08410654B
; Patent No. 5833976
;  GENERAL INFORMATION:
;    APPLICANT:  Rene de Waal Malefyt
;    APPLICANT:  Di-Hwei Hsu
;    APPLICANT:  Anne O'Garra
;    APPLICANT:  Hergen Spits
;    TITLE OF INVENTION:  Use of Interleukin-10 to Treat
;    TITLE OF INVENTION:  Septic Shock
;    NUMBER OF SEQUENCES:  61
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Schering-Plough Corporation
;      STREET:  2000 Galloping Hill Road
;      CITY:  Kenilworth
;      STATE:  New Jersey
;      COUNTRY:  USA
;      ZIP:  07033
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  Macintosh
;      OPERATING SYSTEM:  7.5.3
;      SOFTWARE:  Microsoft Word 5.1a
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/410,654B
;      FILING DATE:  24-MAR-1995
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/229,854
;      FILING DATE:  19-APR-1994
;      APPLICATION NUMBER:  US 07/926,853
;      FILING DATE:  06-AUG-1992
;      APPLICATION NUMBER:  US 07/742,129
;      FILING DATE:  06-AUG-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Foulke, Cynthia L.
;      REGISTRATION NUMBER:  32,364
;      REFERENCE/DOCKET NUMBER:  DX0221KQ1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  908-298-2987
;      TELEFAX:  908-298-5388
;  INFORMATION FOR SEQ ID NO:  42:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  33 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (oligonucleotide)
US-08-410-654B-42

  Query Match             2.0%;  Score 33;  DB 2;  Length 33;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches   33;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     358 GAGAAGTTTTTGAAGAGGGCTGAGAATTCATAA 390
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Db      33 GAGAAGTTTTTGAAGAGGGCTGAGAATTCATAA 1


RESULT 6
US-08-474-851-42/c
; Sequence 42, Application US/08474851
; Patent No. 5837232
;  GENERAL INFORMATION:
;    APPLICANT:  Rene de Waal Malefyt
;    APPLICANT:  Di-Hwei Hsu
;    APPLICANT:  Anne O'Garra
;    APPLICANT:  Hergen Spits
;    TITLE OF INVENTION:  Use of An Interleukin-10 Antagonist to Treat
;    TITLE OF INVENTION:  A B Cell Mediated Autoimmune Disorder
;    NUMBER OF SEQUENCES:  61
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Schering-Plough Corporation
;      STREET:  2000 Galloping Hill Road
;      CITY:  Kenilworth
;      STATE:  New Jersey
;      COUNTRY:  USA
;      ZIP:  07033
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  Macintosh
;      OPERATING SYSTEM:  7.5.3
;      SOFTWARE:  Microsoft Word 6.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/474,851
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/410,654
;      FILING DATE:  24-MAR-1995
;      APPLICATION NUMBER:  US 08/229,854
;      FILING DATE:  19-APR-1994
;      APPLICATION NUMBER:  US 07/926,853
;      FILING DATE:  06-AUG-1992
;      APPLICATION NUMBER:  US 07/742,129
;      FILING DATE:  06-AUG-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Foulke, Cynthia L.
;      REGISTRATION NUMBER:  32,364
;      REFERENCE/DOCKET NUMBER:  DX0221KQ1GD
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  908-298-2987
;      TELEFAX:  908-298-5388
;  INFORMATION FOR SEQ ID NO:  42:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  33 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (oligonucleotide)
US-08-474-851-42

  Query Match             2.0%;  Score 33;  DB 2;  Length 33;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches   33;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     358 GAGAAGTTTTTGAAGAGGGCTGAGAATTCATAA 390
           |||||||||||||||||||||||||||||||||
Db      33 GAGAAGTTTTTGAAGAGGGCTGAGAATTCATAA 1


RESULT 7
US-08-481-560-42/c
; Sequence 42, Application US/08481560
; Patent No. 5837293
;  GENERAL INFORMATION:
;    APPLICANT:  Rene de Waal Malefyt
;    APPLICANT:  Di-Hwei Hsu
;    APPLICANT:  Anne O'Garra
;    APPLICANT:  Hergen Spits
;    TITLE OF INVENTION:  Use of Interleukin-10 to Modulate
;    TITLE OF INVENTION:  Inflammation or T-Cell Mediated
;    TITLE OF INVENTION:  Immune Function
;    NUMBER OF SEQUENCES:  61
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Schering-Plough Corporation
;      STREET:  2000 Galloping Hill Road
```

```
;      CITY:  Kenilworth
;      STATE:  New Jersey
;      COUNTRY:  USA
;      ZIP:  07033
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  Macintosh
;      OPERATING SYSTEM:  7.5.3
;      SOFTWARE:  Microsoft Word 6.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/481,560
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/410,654
;      FILING DATE:  24-MAR-1995
;      APPLICATION NUMBER:  US 08/229,854
;      FILING DATE:  19-APR-1994
;      APPLICATION NUMBER:  US 07/926,853
;      FILING DATE:  06-AUG-1992
;      APPLICATION NUMBER:  US 07/742,129
;      FILING DATE:  06-AUG-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Foulke, Cynthia L.
;      REGISTRATION NUMBER:  32,364
;      REFERENCE/DOCKET NUMBER:  DX0221KQ1GC
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  908-298-2987
;      TELEFAX:  908-298-5388
;  INFORMATION FOR SEQ ID NO:  42:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  33 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (oligonucleotide)
US-08-481-560-42

  Query Match             2.0%;  Score 33;  DB 2;  Length 33;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches   33;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     358 GAGAAGTTTTTGAAGAGGGCTGAGAATTCATAA 390
           |||||||||||||||||||||||||||||||||
Db      33 GAGAAGTTTTTGAAGAGGGCTGAGAATTCATAA 1


RESULT 8
PCT-US96-08142-9/c
; Sequence 9, Application PC/TUS9608142
; GENERAL INFORMATION:
;    APPLICANT:  Constance Emmett, Kimberly A. Foster
;    TITLE OF INVENTION:  Universal Chemistry Enzyme-Linked
;    TITLE OF INVENTION:  Immunosorbent Assay for Detection of
;    TITLE OF INVENTION:  mRNA Expression
;    NUMBER OF SEQUENCES:  9
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Jane Massey Licata, Esq.
;      STREET:  210 Lake Drive East, Suite 201
;      CITY:  Cherry Hill
;      STATE:  NJ
;      COUNTRY:  USA
;      ZIP:  08002
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
;      COMPUTER:  IBM 486
;      OPERATING SYSTEM:  WINDOWS FOR WORKGROUPS
;      SOFTWARE:  WORDPERFECT 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US96/08142
;      FILING DATE:  Herewith
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Jane Massey Licata
;      REGISTRATION NUMBER:  32,257
;      REFERENCE/DOCKET NUMBER:  TCEL-0039
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (609) 779-2400
;      TELEFAX:  (609) 779-8488
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  31
;      TYPE:  Nucleic Acid
;      STRANDEDNESS:  Single
;      TOPOLOGY:  Linear
;    ANTI-SENSE:  No
PCT-US96-08142-9

  Query Match             1.9%;  Score 31;  DB 5;  Length 31;
  Best Local Similarity   100.0%;  Pred. No. 2.8e+02;
  Matches   31;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     119 TGGCAGCCTTCCTGATTTCTGCAGCTCTGTG 149
           |||||||||||||||||||||||||||||||
Db      31 TGGCAGCCTTCCTGATTTCTGCAGCTCTGTG 1


RESULT 9
US-09-308-160B-6/c
; Sequence 6, Application US/09308160B
; Patent No. 6355775
; GENERAL INFORMATION:
;  APPLICANT:  Nagasawa, Yasuo
;  APPLICANT:  Yoshida, Hideaki
;  TITLE OF INVENTION:  TRANSCRIPTIONAL INHIBITOR
;  FILE REFERENCE:  4001-0002
;  CURRENT APPLICATION NUMBER: US/09/308,160B
;  CURRENT FILING DATE:  1999-06-19
;  PRIOR APPLICATION NUMBER:  PCT/JP97/04127
;  PRIOR FILING DATE:  1997-11-12
;  PRIOR APPLICATION NUMBER:  8-305043
;  PRIOR FILING DATE:  1996-11-15
;  NUMBER OF SEQ ID NOS:  31
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 6
;   LENGTH: 30
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-308-160B-6

  Query Match             1.8%;  Score 30;  DB 4;  Length 30;
  Best Local Similarity   100.0%;  Pred. No. 4.5e+02;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      14 GACAGCAGAGCACACAAGCTTCTAGGACAA 43
           ||||||||||||||||||||||||||||||
Db      30 GACAGCAGAGCACACAAGCTTCTAGGACAA 1


RESULT 10
US-09-456-399-6/c
; Sequence 6, Application US/09456399
; Patent No. 6444801
; GENERAL INFORMATION:
;  APPLICANT:  Institute of Cytosignal Research, Inc.
;  TITLE OF INVENTION:  Transcriptional Inhibitor
;  FILE REFERENCE:  S1-802PCT-US
;  CURRENT APPLICATION NUMBER: US/09/456,399
;  CURRENT FILING DATE:  1999-12-08
;  PRIOR APPLICATION NUMBER:  JP   1996-305043
;  PRIOR FILING DATE:  1996-11-15
```

```
;  PRIOR APPLICATION NUMBER:  PCT/JP97/04127
;  PRIOR FILING DATE:  1997-11-12
;  PRIOR APPLICATION NUMBER:  US 09/308,160
;  PRIOR FILING DATE:  1999-05-14
;  NUMBER OF SEQ ID NOS:  15
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 6
;   LENGTH: 30
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:an artificially
;   OTHER INFORMATION: synthesized primer sequence
US-09-456-399-6

  Query Match             1.8%;  Score 30;  DB 4;  Length 30;
  Best Local Similarity   100.0%;  Pred. No. 4.5e+02;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      14 GACAGCAGAGCACACAAGCTTCTAGGACAA 43
           ||||||||||||||||||||||||||||||
Db      30 GACAGCAGAGCACACAAGCTTCTAGGACAA 1


RESULT 11
US-08-859-998-479
; Sequence 479, Application US/08859998
; Patent No. 5994076
;  GENERAL INFORMATION:
;    APPLICANT:  Chenchik, Alex
;    APPLICANT:  Jokhadze, George
;    APPLICANT:  Bibilashvilli, Robert
;    TITLE OF INVENTION:  METHOD OF ASSAYING DIFFERENTIAL
;    TITLE OF INVENTION:  EXPRESSION
;    NUMBER OF SEQUENCES:  1375
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fish & Richardson, P.C.
;      STREET:  2200 Sand Hill Road, Suite 100
;      CITY:  Menlo Park
;      STATE:  CA
;      COUNTRY:  US
;      ZIP:  94025
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  Windows95
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/859,998
;      FILING DATE:  21-MAY-1997
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Field, Bret E.
;      REGISTRATION NUMBER:  37,620
;      REFERENCE/DOCKET NUMBER:  09096/002001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-322-5070
;      TELEFAX:  415-854-0875
;  INFORMATION FOR SEQ ID NO:  479:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  28 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA
;    FEATURE:
;      OTHER INFORMATION:  oligonucleotide primer
US-08-859-998-479

  Query Match             1.7%;  Score 28;  DB 2;  Length 28;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+03;
  Matches   28;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      88 AACATGACTTCCAAGCTGGCCGTGGCTC 115
           ||||||||||||||||||||||||||||
Db       1 AACATGACTTCCAAGCTGGCCGTGGCTC 28


RESULT 12
US-08-859-998-480/c
; Sequence 480, Application US/08859998
; Patent No. 5994076
;  GENERAL INFORMATION:
;    APPLICANT:  Chenchik, Alex
;    APPLICANT:  Jokhadze, George
;    APPLICANT:  Bibilashvilli, Robert
;    TITLE OF INVENTION:  METHOD OF ASSAYING DIFFERENTIAL
;    TITLE OF INVENTION:  EXPRESSION
;    NUMBER OF SEQUENCES:  1375
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fish & Richardson, P.C.
;      STREET:  2200 Sand Hill Road, Suite 100
;      CITY:  Menlo Park
;      STATE:  CA
;      COUNTRY:  US
;      ZIP:  94025
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  Windows95
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/859,998
;      FILING DATE:  21-MAY-1997
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Field, Bret E.
;      REGISTRATION NUMBER:  37,620
;      REFERENCE/DOCKET NUMBER:  09096/002001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-322-5070
;      TELEFAX:  415-854-0875
;  INFORMATION FOR SEQ ID NO:  480:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  28 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA
;    FEATURE:
;      OTHER INFORMATION:  oligonucleotide primer
US-08-859-998-480

  Query Match             1.7%;  Score 28;  DB 2;  Length 28;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+03;
  Matches   28;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     248 GAGTGATTGAGAGTGGACCACACTGCGC 275
           ||||||||||||||||||||||||||||
Db      28 GAGTGATTGAGAGTGGACCACACTGCGC 1


RESULT 13
US-09-225-928-479
; Sequence 479, Application US/09225928
; Patent No. 6352829
;  GENERAL INFORMATION:
;       APPLICANT: Chenchik, Alex
;                  Jokhadze, George
;                  Bibilashvilli, Robert
```

```
;       TITLE OF INVENTION: METHOD OF ASSAYING DIFFERENTIAL
;                           EXPRESSION
;       NUMBER OF SEQUENCES: 1375
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Fish & Richardson, P.C.
;            STREET: 2200 Sand Hill Road, Suite 100
;            CITY: Menlo Park
;            STATE: CA
;            COUNTRY: US
;            ZIP: 94025
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Diskette
;            COMPUTER: IBM Compatible
;            OPERATING SYSTEM: Windows95
;            SOFTWARE: FastSEQ for Windows Version 2.0
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/225,928
;            FILING DATE: 05-Jan-1999
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 08/859,998
;            FILING DATE: 21-MAY-1997
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Field, Bret E.
;            REGISTRATION NUMBER: 37,620
;            REFERENCE/DOCKET NUMBER: 09096/002001
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 415-322-5070
;            TELEFAX: 415-854-0875
;   INFORMATION FOR SEQ ID NO: 479:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 28 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       MOLECULE TYPE: DNA
;       FEATURE:
;            OTHER INFORMATION: oligonucleotide primer
;       SEQUENCE DESCRIPTION: SEQ ID NO: 479:
US-09-225-928-479

  Query Match             1.7%;  Score 28;  DB 4;  Length 28;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+03;
  Matches   28;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      88 AACATGACTTCCAAGCTGGCCGTGGCTC 115
           ||||||||||||||||||||||||||||
Db       1 AACATGACTTCCAAGCTGGCCGTGGCTC 28


RESULT 14
US-09-225-928-480/c
; Sequence 480, Application US/09225928
; Patent No. 6352829
;   GENERAL INFORMATION:
;       APPLICANT: Chenchik, Alex
;                  Jokhadze, George
;                  Bibilashvilli, Robert
;       TITLE OF INVENTION: METHOD OF ASSAYING DIFFERENTIAL
;                           EXPRESSION
;       NUMBER OF SEQUENCES: 1375
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Fish & Richardson, P.C.
;            STREET: 2200 Sand Hill Road, Suite 100
;            CITY: Menlo Park
;            STATE: CA
;            COUNTRY: US
;            ZIP: 94025
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Diskette
;            COMPUTER: IBM Compatible
;            OPERATING SYSTEM: Windows95
;            SOFTWARE: FastSEQ for Windows Version 2.0
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/225,928
;            FILING DATE: 05-Jan-1999
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 08/859,998
;            FILING DATE: 21-MAY-1997
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Field, Bret E.
;            REGISTRATION NUMBER: 37,620
;            REFERENCE/DOCKET NUMBER: 09096/002001
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 415-322-5070
;            TELEFAX: 415-854-0875
;   INFORMATION FOR SEQ ID NO: 480:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 28 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       MOLECULE TYPE: DNA
;       FEATURE:
;            OTHER INFORMATION: oligonucleotide primer
;       SEQUENCE DESCRIPTION: SEQ ID NO: 480:
US-09-225-928-480

  Query Match             1.7%;  Score 28;  DB 4;  Length 28;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+03;
  Matches   28;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     248 GAGTGATTGAGAGTGGACCACACTGCGC 275
           ||||||||||||||||||||||||||||
Db      28 GAGTGATTGAGAGTGGACCACACTGCGC 1


RESULT 15
US-08-327-494A-8/c
; Sequence 8, Application US/08327494A
; Patent No. 5527678
;  GENERAL INFORMATION:
;    APPLICANT:  Blaser, Martin J.
;    APPLICANT:  Tummuru, Murali K.R.
;    APPLICANT:  Sharma, Smita A
;    TITLE OF INVENTION:  cagB and cagC Genes for H. pylori and
;    TITLE OF INVENTION:  Related Methods and Compositions
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  NEEDLE & ROSENBERG, P.C.
;      STREET:  127 Peachtree Street, Suite 1200
;      CITY:  Atlanta
;      STATE:  Georgia
;      COUNTRY:  USA
;      ZIP:  303-3
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/327,494A
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Spratt, Gwendolyn D.
;      REGISTRATION NUMBER:  36,016
;      REFERENCE/DOCKET NUMBER:  2200.029
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  404/688-0770
;      TELEFAX:  404/688-9880
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  25 base pairs
;      TYPE:  nucleic acid
```

```
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  DNA (genomic)
US-08-327-494A-8

  Query Match             1.5%;  Score 25;  DB 1;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 4.6e+03;
  Matches   25;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     358 GAGAAGTTTTTGAAGAGGGCTGAGA 382
           |||||||||||||||||||||||||
Db      25 GAGAAGTTTTTGAAGAGGGCTGAGA 1


RESULT 16
PCT-US95-13659-8/c
; Sequence 8, Application PC/TUS9513659
;  GENERAL INFORMATION:
;     APPLICANT:  Blaser, Martin J.
;     APPLICANT:  Tummuru, Murali K.R.
;     APPLICANT:  Sharma, Smita A
;     TITLE OF INVENTION:  cagB and cagC Genes for H. pylori and
;     TITLE OF INVENTION:  Related Methods and Compositions
;     NUMBER OF SEQUENCES:  8
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  NEEDLE & ROSENBERG, P.C.
;       STREET:  127 Peachtree Street, Suite 1200
;       CITY:  Atlanta
;       STATE:  Georgia
;       COUNTRY:  USA
;       ZIP:  303-3
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  PCT/US95/13659
;       FILING DATE:
;       CLASSIFICATION:
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Spratt, Gwendolyn D.
;       REGISTRATION NUMBER:  36,016
;       REFERENCE/DOCKET NUMBER:  2200.029
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  404/688-0770
;       TELEFAX:  404/688-9880
;   INFORMATION FOR SEQ ID NO:  8:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  25 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  DNA (genomic)
PCT-US95-13659-8

  Query Match             1.5%;  Score 25;  DB 5;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 4.6e+03;
  Matches   25;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     358 GAGAAGTTTTTGAAGAGGGCTGAGA 382
           |||||||||||||||||||||||||
Db      25 GAGAAGTTTTTGAAGAGGGCTGAGA 1


RESULT 17
PCT-US96-08142-8/c
; Sequence 8, Application PC/TUS9608142
;  GENERAL INFORMATION:
;     APPLICANT:  Constance Emmett, Kimberly A. Foster
;     TITLE OF INVENTION:  Universal Chemistry Enzyme-Linked
;     TITLE OF INVENTION:  Immunosorbent Assay for Detection of
;     TITLE OF INVENTION:  mRNA Expression
;     NUMBER OF SEQUENCES:  9
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Jane Massey Licata, Esq.
;       STREET:  210 Lake Drive East, Suite 201
;       CITY:  Cherry Hill
;       STATE:  NJ
;       COUNTRY:  USA
;       ZIP:  08002
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
;       COMPUTER:  IBM 486
;       OPERATING SYSTEM:  WINDOWS FOR WORKGROUPS
;       SOFTWARE:  WORDPERFECT 5.1
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  PCT/US96/08142
;       FILING DATE:  Herewith
;       CLASSIFICATION:
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:
;       FILING DATE:
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Jane Massey Licata
;       REGISTRATION NUMBER:  32,257
;       REFERENCE/DOCKET NUMBER:  TCEL-0039
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (609) 779-2400
;       TELEFAX:  (609) 779-8488
;   INFORMATION FOR SEQ ID NO:  8:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  25
;       TYPE:  Nucleic Acid
;       STRANDEDNESS:  Single
;       TOPOLOGY:  Linear
;     ANTI-SENSE:  No
PCT-US96-08142-8

  Query Match             1.5%;  Score 25;  DB 5;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 4.6e+03;
  Matches   25;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     358 GAGAAGTTTTTGAAGAGGGCTGAGA 382
           |||||||||||||||||||||||||
Db      25 GAGAAGTTTTTGAAGAGGGCTGAGA 1


RESULT 18
US-09-710-200-72/c
; Sequence 72, Application US/09710200
; Patent No. 6379897
; GENERAL INFORMATION:
;  APPLICANT: Nanogen, Inc.
;  APPLICANT:  Weidenhammer, Elaine M.
;  APPLICANT:  Wang, Ling
;  APPLICANT:  Xu, Xiao
;  APPLICANT:  Heller, Michael J.
;  APPLICANT:  Kahl, Brenda F.
;  TITLE OF INVENTION: IMPROVED METHODS FOR GENE EXPRESSION MONITORING ON ELECTRONIC
;  FILE REFERENCE: 256/262 Patrick S. Eagleman
;  CURRENT APPLICATION NUMBER: US/09/710,200
;  CURRENT FILING DATE:  2000-11-09
;  NUMBER OF SEQ ID NOS: 73
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 72
;   LENGTH: 24
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-710-200-72

  Query Match             1.5%;  Score 24;  DB 4;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 7.2e+03;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     475 GTGTGGGTCTGTTGTAGGGTTGCC 498
```

```
          ||||||||||||||||||||||||
Db      24 GTGTGGGTCTGTTGTAGGGTTGCC 1


RESULT 19
PCT-US96-08142-7
; Sequence 7, Application PC/TUS9608142
;  GENERAL INFORMATION:
;    APPLICANT:  Constance Emmett, Kimberly A. Foster
;    TITLE OF INVENTION:  Universal Chemistry Enzyme-Linked
;    TITLE OF INVENTION:  Immunosorbent Assay for Detection of
;    TITLE OF INVENTION:  mRNA Expression
;    NUMBER OF SEQUENCES:  9
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Jane Massey Licata, Esq.
;      STREET:  210 Lake Drive East, Suite 201
;      CITY:  Cherry Hill
;      STATE:  NJ
;      COUNTRY:  USA
;      ZIP:  08002
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
;      COMPUTER:  IBM 486
;      OPERATING SYSTEM:  WINDOWS FOR WORKGROUPS
;      SOFTWARE:  WORDPERFECT 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US96/08142
;      FILING DATE:  Herewith
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Jane Massey Licata
;      REGISTRATION NUMBER:  32,257
;      REFERENCE/DOCKET NUMBER:  TCEL-0039
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (609) 779-2400
;      TELEFAX:  (609) 779-8488
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  24
;      TYPE:  Nucleic Acid
;      STRANDEDNESS:  Single
;      TOPOLOGY:  Linear
;    ANTI-SENSE:  No
PCT-US96-08142-7

  Query Match             1.5%;  Score 24;  DB 5;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 7.2e+03;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      91 ATGACTTCCAAGCTGGCCGTGGCT 114
           ||||||||||||||||||||||||
Db       1 ATGACTTCCAAGCTGGCCGTGGCT 24


RESULT 20
US-09-641-638-1167/c
; Sequence 1167, Application US/09641638
; Patent No. 6432648
; GENERAL INFORMATION:
;  APPLICANT:  Blumenfeld, Marta
;  APPLICANT:  Bougueleret, Lydie
;  APPLICANT:  Chumakov, Ilya
;  APPLICANT:  Cohen, Annick
;  TITLE OF INVENTION:  BIALLELIC MARKERS DERIVED FROM GENOMIC REGIONS CARRYING
;  TITLE OF INVENTION:  GENES INVOLVED IN ARACHIDONIC ACID METABOLISM
;  FILE REFERENCE:  GENSET.051CP1
;  CURRENT APPLICATION NUMBER: US/09/641,638
;  CURRENT FILING DATE:  2000-08-16
;  PRIOR APPLICATION NUMBER:  US 09/502,330
;  PRIOR FILING DATE:  2000-02-11
;  PRIOR APPLICATION NUMBER:  US 60/133,200
;  PRIOR FILING DATE:  1999-05-07
;  PRIOR APPLICATION NUMBER:  US 09/275,267
;  PRIOR FILING DATE:  1999-03-23
;  PRIOR APPLICATION NUMBER:  US 60/119,917
;  PRIOR FILING DATE:  1999-02-12
;  NUMBER OF SEQ ID NOS:  1304
;  SOFTWARE:  Patent.pm
; SEQ ID NO 1167
;   LENGTH: 47
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
;   FEATURE:
;   NAME/KEY: allele
;   LOCATION: 24
;   OTHER INFORMATION: 12-564-214 : polymorphic base C or T
US-09-641-638-1167

  Query Match             1.4%;  Score 23.4;  DB 4;  Length 47;
  Best Local Similarity   69.8%;  Pred. No. 1.1e+04;
  Matches   30;  Conservative    1;  Mismatches   12;  Indels    0;  Gaps    0;

Qy    1256 AACAAATAATTTTTTAGTATAAGTACATTATTGTTTATCTGAA 1298
           || ||||||||   ||| | ||: | | | || || |||||||
Db      46 AAAAAATAATTAAATAGAAGAARAAAACTGTTCTTCATCTGAA 4


Search completed: February  9, 2003, 19:22:03
Job time : 103 secs
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GenCore version 5.1.3

OM nucleic - nucleic search, using sw model

Run on: February 9, 2003, 17:25:52 ; Search time 133 Seconds
(without alignments)
5841.285 Million cell updates/sec

Title: US-09-960-143-3
Perfect score: 1639
Sequence: 1 acaaactttcagagacagca.....atataatttgttgtcaaagt 1639

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 408267 seqs, 237001491 residues

Total number of hits satisfying chosen parameters: 231544

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA:*
1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
10: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
11: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
12: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
13: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	30.6	1.9	31	10	US-09-801-274-1358	Sequence 1358, Ap
c 2	30	1.8	30	10	US-09-816-124-4	Sequence 4, Appli
c 3	25	1.5	25	10	US-09-885-441-31	Sequence 31, Appl
c 4	24	1.5	24	10	US-09-975-408-72	Sequence 72, Appl
c 5	24	1.5	24	12	US-10-075-579-72	Sequence 72, Appl
c 6	21.8	1.3	47	9	US-09-853-526-250	Sequence 250, App
c 7	21.8	1.3	47	9	US-09-853-526-327	Sequence 327, App
c 8	21.8	1.3	47	10	US-09-901-484A-250	Sequence 250, App
c 9	21.8	1.3	47	10	US-09-901-484A-327	Sequence 327, App
10	21.6	1.3	41	10	US-09-955-462A-1	Sequence 1, Appli
11	20.4	1.2	34	10	US-09-955-462A-2	Sequence 2, Appli
12	20.4	1.2	48	9	US-09-864-785-3472	Sequence 3472, Ap
13	20.2	1.2	48	9	US-09-864-785-3568	Sequence 3568, Ap
c 14	20	1.2	20	10	US-09-975-408-73	Sequence 73, Appl
c 15	20	1.2	20	12	US-10-075-579-73	Sequence 73, Appl
c 16	20	1.2	28	10	US-09-142-593-40	Sequence 40, Appl
17	20	1.2	48	9	US-09-864-785-3460	Sequence 3460, Ap
18	19.8	1.2	43	9	US-09-828-523A-96	Sequence 96, Appl
19	19.8	1.2	48	9	US-09-825-805-64	Sequence 64, Appl
c 20	19.6	1.2	45	9	US-10-017-736-9	Sequence 9, Appli
21	19.4	1.2	49	10	US-09-773-385-3	Sequence 3, Appli
22	19.4	1.2	50	9	US-09-992-598-45	Sequence 45, Appl
23	19.4	1.2	50	9	US-09-989-293A-45	Sequence 45, Appl
24	19.4	1.2	50	9	US-09-989-735-45	Sequence 45, Appl
25	19.4	1.2	50	9	US-09-990-444-45	Sequence 45, Appl
26	19.4	1.2	50	9	US-09-989-730-45	Sequence 45, Appl
27	19.4	1.2	50	9	US-09-990-436-45	Sequence 45, Appl
28	19.4	1.2	50	9	US-09-991-181-45	Sequence 45, Appl
29	19.4	1.2	50	9	US-09-993-687-45	Sequence 45, Appl
30	19.4	1.2	50	9	US-09-989-734-45	Sequence 45, Appl
31	19.4	1.2	50	9	US-09-997-653-45	Sequence 45, Appl
32	19.4	1.2	50	9	US-09-993-667-45	Sequence 45, Appl
33	19.4	1.2	50	10	US-09-989-722-45	Sequence 45, Appl
34	19.4	1.2	50	10	US-09-989-723-45	Sequence 45, Appl
35	19.4	1.2	50	10	US-09-989-279-45	Sequence 45, Appl
36	19.4	1.2	50	10	US-09-989-727-45	Sequence 45, Appl
37	19.4	1.2	50	10	US-09-989-731-45	Sequence 45, Appl
38	19.4	1.2	50	10	US-09-989-732-45	Sequence 45, Appl
39	19.4	1.2	50	10	US-09-991-073-45	Sequence 45, Appl
40	19.4	1.2	50	10	US-09-990-442-45	Sequence 45, Appl
41	19.4	1.2	50	10	US-09-991-163-45	Sequence 45, Appl
42	19.4	1.2	50	10	US-09-993-604-45	Sequence 45, Appl
43	19.4	1.2	50	10	US-09-990-456-45	Sequence 45, Appl
44	19.4	1.2	50	10	US-09-989-721-45	Sequence 45, Appl
45	19.2	1.2	24	10	US-09-885-441-30	Sequence 30, Appl

ALIGNMENTS

RESULT 1
US-09-801-274-1358
; Sequence 1358, Application US/09801274
; Patent No. US20020032319A1
; GENERAL INFORMATION:
; APPLICANT: Cargill, Michele
; APPLICANT: Ireland, James S.
; APPLICANT: Lander, Eric S.
; TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS
; FILE REFERENCE: 2825.2009-001
; CURRENT APPLICATION NUMBER: US/09/801,274
; CURRENT FILING DATE: 2001-03-07
; PRIOR APPLICATION NUMBER: US 60/187,510
; PRIOR FILING DATE: 2000-03-07
; PRIOR APPLICATION NUMBER: US 60/206,129
; PRIOR FILING DATE: 2000-05-22
; NUMBER OF SEQ ID NOS: 1802
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1358
; LENGTH: 31
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-801-274-1358

Query Match 1.9%; Score 30.6; DB 10; Length 31;
Best Local Similarity 96.8%; Pred. No. 2.4e+03;
Matches 30; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 220 TTCCACCCCAAATTTATCAAAGAACTGAGAG 250
||||||||||||||||:|||||||||||||||
Db 1 TTCCACCCCAAATTTMTCAAAGAACTGAGAG 31

RESULT 2
US-09-816-124-4/c
; Sequence 4, Application US/09816124
; Patent No. US20020150897A1
; GENERAL INFORMATION:
; APPLICANT: Nagasawa, Yasuo
; APPLICANT: Yoshida, Hideaki
; TITLE OF INVENTION: Method for detecting and isolating genes
; FILE REFERENCE: S1-801PCT

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;  CURRENT APPLICATION NUMBER: US/09/816,124
;  CURRENT FILING DATE:  2001-03-26
;  PRIOR APPLICATION NUMBER: PCT/JP97/04126
;  PRIOR FILING DATE: 1997-11-12
;  PRIOR APPLICATION NUMBER: JP 1996-305163
;  PRIOR FILING DATE: 1996-11-15
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
;   LENGTH: 30
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Artificially synthesized primer sequence
US-09-816-124-4

  Query Match             1.8%;  Score 30;  DB 10;  Length 30;
  Best Local Similarity   100.0%;  Pred. No. 3e+03;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      14 GACAGCAGAGCACACAAGCTTCTAGGACAA 43
           ||||||||||||||||||||||||||||||
Db      30 GACAGCAGAGCACACAAGCTTCTAGGACAA 1


RESULT 3
US-09-885-441-31/c
; Sequence 31, Application US/09885441
; Patent No. US20020146407A1
; GENERAL INFORMATION:
;  APPLICANT: Xiao, Yonghong
;  TITLE OF INVENTION: Regulation of Human Eosinophil Serine
;  TITLE OF INVENTION:  Protease-1-Like Enzyme
;  FILE REFERENCE: 04974.00512
;  CURRENT APPLICATION NUMBER: US/09/885,441
;  CURRENT FILING DATE:  2001-06-21
;  PRIOR APPLICATION NUMBER: US 60/212,844
;  PRIOR FILING DATE: 2000-06-21
;  PRIOR APPLICATION NUMBER: US 60/244,171
;  PRIOR FILING DATE: 2000-10-31
;  PRIOR APPLICATION NUMBER: US 60/279,766
;  PRIOR FILING DATE: 2001-03-30
;  PRIOR APPLICATION NUMBER: PCT/_____
;  PRIOR FILING DATE: 2001-06-20
;  NUMBER OF SEQ ID NOS: 58
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 31
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-885-441-31

  Query Match             1.5%;  Score 25;  DB 10;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+04;
  Matches   25;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     888 TGTTCCACTGTGCCTTGGTTTCTCC 912
           |||||||||||||||||||||||||
Db      25 TGTTCCACTGTGCCTTGGTTTCTCC 1


RESULT 4
US-09-975-408-72/c
; Sequence 72, Application US/09975408
; Patent No. US20020150917A1
; GENERAL INFORMATION:
;  APPLICANT: Nanogen, Inc.
;  APPLICANT:  Weidenhammer, Elaine M.
;  APPLICANT:  Xu, Xiao
;  APPLICANT:  Kahl, Brenda F.
;  TITLE OF INVENTION: IMPROVED METHODS FOR GENE EXPRESSION MONITORING ON ELECTRONIC MIC
;  FILE REFERENCE: 267/174  Patrick S. Eagleman
;  CURRENT APPLICATION NUMBER: US/09/975,408
;  CURRENT FILING DATE:  2001-10-10
;  PRIOR APPLICATION NUMBER: 09/710,200
;  PRIOR FILING DATE: 2000-11-09
;  NUMBER OF SEQ ID NOS: 73
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 72
;   LENGTH: 24
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-975-408-72

  Query Match             1.5%;  Score 24;  DB 10;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 3.3e+04;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     475 GTGTGGGTCTGTTGTAGGGTTGCC 498
           ||||||||||||||||||||||||
Db      24 GTGTGGGTCTGTTGTAGGGTTGCC 1


RESULT 5
US-10-075-579-72/c
; Sequence 72, Application US/10075579
; Patent No. US20020119484A1
; GENERAL INFORMATION:
;  APPLICANT: Nanogen, Inc.
;  APPLICANT:  Weidenhammer, Elaine M.
;  APPLICANT:  Wang, Ling
;  APPLICANT:  Xu, Xiao
;  APPLICANT:  Heller, Michael J.
;  APPLICANT:  Kahl, Brenda F.
;  TITLE OF INVENTION: IMPROVED METHODS FOR GENE EXPRESSION MONITORING ON ELECTRONIC
;  FILE REFERENCE: 256/262 Patrick S. Eagleman
;  CURRENT APPLICATION NUMBER: US/10/075,579
;  CURRENT FILING DATE:  2002-02-12
;  PRIOR APPLICATION NUMBER: US/09/710,200
;  PRIOR FILING DATE: 2000-11-09
;  NUMBER OF SEQ ID NOS: 73
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 72
;   LENGTH: 24
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-075-579-72

  Query Match             1.5%;  Score 24;  DB 12;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 3.3e+04;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     475 GTGTGGGTCTGTTGTAGGGTTGCC 498
           ||||||||||||||||||||||||
Db      24 GTGTGGGTCTGTTGTAGGGTTGCC 1


RESULT 6
US-09-853-526-250/c
; Sequence 250, Application US/09853526
; Patent No. US20020165345A1
; GENERAL INFORMATION:
;  APPLICANT: Cohen, Daniel
;  APPLICANT:  Blumenfeld, Marta
;  APPLICANT:  Ilya, Chumakov
;  APPLICANT:  Bougueleret, Lydie
;  TITLE OF INVENTION: PROSTATE CANCER GENE
;  FILE REFERENCE: GENSET.18CP1CP
;  CURRENT APPLICATION NUMBER: US/09/853,526
;  CURRENT FILING DATE:  2001-05-11
;  PRIOR APPLICATION NUMBER: 09/338,907
;  PRIOR FILING DATE: 1999-06-23
;  PRIOR APPLICATION NUMBER: 08/996,306
;  PRIOR FILING DATE: 1997-12-22
;  PRIOR APPLICATION NUMBER: 60/099,658
;  PRIOR FILING DATE: 1998-09-09
```

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;  PRIOR APPLICATION NUMBER: 09/218,207
;  PRIOR FILING DATE: 1998-12-22
;  NUMBER OF SEQ ID NOS: 578
;  SOFTWARE: Patent.pm
; SEQ ID NO 250
;   LENGTH: 47
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
;   FEATURE:
;   NAME/KEY: allele
;   LOCATION: 1..47
;   OTHER INFORMATION: polymorphic fragment 99-1480-290
;   NAME/KEY: allele
;   LOCATION: 24
;   OTHER INFORMATION: polymorphic base G
;   NAME/KEY: primer_bind
;   LOCATION: 1..23
;   OTHER INFORMATION: potential microsequencing oligo 99-1480-290.mis1
;   NAME/KEY: primer_bind
;   LOCATION: 25..47
;   OTHER INFORMATION: complement potential microsequencing oligo 99-1480-290.mis2
US-09-853-526-250

  Query Match             1.3%;  Score 21.8;  DB 9;  Length 47;
  Best Local Similarity   70.7%;  Pred. No. 9.1e+04;
  Matches   29;  Conservative    0;  Mismatches   12;  Indels    0;  Gaps    0;

Qy     331 AAGGAAAACTGGGTGCAGAGGGTTGTGGAGAAGTTTTTGAA 371
           |||||  | ||| |||   |||||||||| |||| |  || |
Db      41 AAGGATCAGTGGTTGCCCGGGGTTGTGGTGAAGATGGTGCA 1


RESULT 7
US-09-853-526-327/c
; Sequence 327, Application US/09853526
; Patent No. US20020165345A1
; GENERAL INFORMATION:
;  APPLICANT: Cohen, Daniel
;  APPLICANT:  Blumenfeld, Marta
;  APPLICANT:  Ilya, Chumakov
;  APPLICANT:  Bougueleret, Lydie
;  TITLE OF INVENTION: PROSTATE CANCER GENE
;  FILE REFERENCE: GENSET.18CP1CP
;  CURRENT APPLICATION NUMBER: US/09/853,526
;  CURRENT FILING DATE:  2001-05-11
;  PRIOR APPLICATION NUMBER: 09/338,907
;  PRIOR FILING DATE: 1999-06-23
;  PRIOR APPLICATION NUMBER: 08/996,306
;  PRIOR FILING DATE: 1997-12-22
;  PRIOR APPLICATION NUMBER: 60/099,658
;  PRIOR FILING DATE: 1998-09-09
;  PRIOR APPLICATION NUMBER: 09/218,207
;  PRIOR FILING DATE: 1998-12-22
;  NUMBER OF SEQ ID NOS: 578
;  SOFTWARE: Patent.pm
; SEQ ID NO 327
;   LENGTH: 47
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
;   FEATURE:
;   NAME/KEY: allele
;   LOCATION: 1..47
;   OTHER INFORMATION: polymorphic fragment 99-1480-290, variant version of SEQ ID250
;   NAME/KEY: allele
;   LOCATION: 24
;   OTHER INFORMATION: base T ; G in SEQ ID250
;   NAME/KEY: primer_bind
;   LOCATION: 1..23
;   OTHER INFORMATION: potential microsequencing oligo 99-1480-290.mis1
;   NAME/KEY: primer_bind
;   LOCATION: 25..47
;   OTHER INFORMATION: complement potential microsequencing oligo 99-1480-290.mis2
US-09-853-526-327

  Query Match             1.3%;  Score 21.8;  DB 9;  Length 47;
  Best Local Similarity   70.7%;  Pred. No. 9.1e+04;
  Matches   29;  Conservative    0;  Mismatches   12;  Indels    0;  Gaps    0;

Qy     331 AAGGAAAACTGGGTGCAGAGGGTTGTGGAGAAGTTTTTGAA 371
           |||||  | ||| |||   |||||||||| |||| |  || |
Db      41 AAGGATCAGTGGTTGCCAGGGGTTGTGGTGAAGATGGTGCA 1


RESULT 8
US-09-901-484A-250/c
; Sequence 250, Application US/09901484A
; Patent No. US20020119460A1
; GENERAL INFORMATION:
;  APPLICANT: Cohen, Daniel
;  APPLICANT:  Blumenfeld, Marta
;  APPLICANT:  Chumakov, Ilya
;  APPLICANT:  Bougueleret, Lydie
;  TITLE OF INVENTION: Prostate Cancer Gene
;  FILE REFERENCE: GEN-T111XC3D2
;  CURRENT APPLICATION NUMBER: US/09/901,484A
;  CURRENT FILING DATE:  2001-07-09
;  PRIOR APPLICATION NUMBER: US 08/996,306
;  PRIOR FILING DATE: 1997-12-22
;  PRIOR APPLICATION NUMBER: US 60/099,658
;  PRIOR FILING DATE: 1998-09-09
;  PRIOR APPLICATION NUMBER: US 09/218,207
;  PRIOR FILING DATE: 1998-12-22
;  PRIOR APPLICATION NUMBER: US 09/338,907
;  PRIOR FILING DATE: 1999-06-23
;  PRIOR APPLICATION NUMBER: US 09/853,526
;  PRIOR FILING DATE: 2001-05-11
;  NUMBER OF SEQ ID NOS: 578
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 250
;   LENGTH: 47
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: allele
;   LOCATION: (1)..(47)
;   OTHER INFORMATION: polymorphic fragment 99-1480-290
;   NAME/KEY: allele
;   LOCATION: (24)..(24)
;   OTHER INFORMATION: polymorphic base G
;   NAME/KEY: primer_bind
;   LOCATION: (1)..(23)
;   OTHER INFORMATION: potential microsequencing oligo 99-1480-290.mis1
;   NAME/KEY: primer_bind
;   LOCATION: (25)..(47)
;   OTHER INFORMATION: complement potential microsequencing oligo 99-1480-290.mis2
US-09-901-484A-250

  Query Match             1.3%;  Score 21.8;  DB 10;  Length 47;
  Best Local Similarity   70.7%;  Pred. No. 9.1e+04;
  Matches   29;  Conservative    0;  Mismatches   12;  Indels    0;  Gaps    0;

Qy     331 AAGGAAAACTGGGTGCAGAGGGTTGTGGAGAAGTTTTTGAA 371
           |||||  | ||| |||   |||||||||| |||| |  || |
Db      41 AAGGATCAGTGGTTGCCCGGGGTTGTGGTGAAGATGGTGCA 1


RESULT 9
US-09-901-484A-327/c
; Sequence 327, Application US/09901484A
; Patent No. US20020119460A1
; GENERAL INFORMATION:
;  APPLICANT: Cohen, Daniel
;  APPLICANT:  Blumenfeld, Marta
;  APPLICANT:  Chumakov, Ilya
;  APPLICANT:  Bougueleret, Lydie
;  TITLE OF INVENTION: Prostate Cancer Gene
```

```
;  FILE REFERENCE: GEN-T111XC3D2
;  CURRENT APPLICATION NUMBER: US/09/901,484A
;  CURRENT FILING DATE:  2001-07-09
;  PRIOR APPLICATION NUMBER: US 08/996,306
;  PRIOR FILING DATE: 1997-12-22
;  PRIOR APPLICATION NUMBER: US 60/099,658
;  PRIOR FILING DATE: 1998-09-09
;  PRIOR APPLICATION NUMBER: US 09/218,207
;  PRIOR FILING DATE: 1998-12-22
;  PRIOR APPLICATION NUMBER: US 09/338,907
;  PRIOR FILING DATE: 1999-06-23
;  PRIOR APPLICATION NUMBER: US 09/853,526
;  PRIOR FILING DATE: 2001-05-11
;  NUMBER OF SEQ ID NOS: 578
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 327
;   LENGTH: 47
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: allele
;   LOCATION: (1)..(47)
;   OTHER INFORMATION: polymorphic fragment 99-1480-290, variant version of SEQ ID 250
;   NAME/KEY: allele
;   LOCATION: (24)..(24)
;   OTHER INFORMATION: polymorphic base T; G in SEQ ID 250
;   NAME/KEY: primer_bind
;   LOCATION: (1)..(23)
;   OTHER INFORMATION: potential microsequencing oligo 99-1480-290.mis1
;   NAME/KEY: primer_bind
;   LOCATION: (25)..(47)
;   OTHER INFORMATION: complement potential microsequencing oligo 99-1480-290.mis2
US-09-901-484A-327

  Query Match             1.3%;  Score 21.8;  DB 10;  Length 47;
  Best Local Similarity   70.7%;  Pred. No. 9.1e+04;
  Matches   29;  Conservative    0;  Mismatches   12;  Indels    0;  Gaps    0;

Qy     331 AAGGAAAACTGGGTGCAGAGGGTTGTGGAGAAGTTTTTGAA 371
           |||||  | ||| ||| ' |||||||| |||| |  || |
Db      41 AAGGATCAGTGGTTGCCAGGGGTTGTGGTGAAGATGGTGCA 1


RESULT 10
US-09-955-462A-1
; Sequence 1, Application US/09955462A
; Patent No. US20020150913A1
; GENERAL INFORMATION:
;  APPLICANT: Wilusz, Jeffrey
;  APPLICANT:  Wilusz, Carol
;  APPLICANT:  Gao, Min
;  TITLE OF INVENTION: Compositions and Methods for Reproducing and Modulating Mammalian
;  TITLE OF INVENTION:  Messenger RNA Decapping
;  FILE REFERENCE: 601-1-109N
;  CURRENT APPLICATION NUMBER: US/09/955,462A
;  CURRENT FILING DATE:  2002-04-30
;  PRIOR APPLICATION NUMBER: US 60/233,682
;  PRIOR FILING DATE: 2000-09-19
;  NUMBER OF SEQ ID NOS: 3
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
;   LENGTH: 41
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: described in specification page 28
US-09-955-462A-1

  Query Match             1.3%;  Score 21.6;  DB 10;  Length 41;
  Best Local Similarity   85.7%;  Pred. No. 9.6e+04;
  Matches   24;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy    1038 TATTTATTATTTATGTATTTATTTAAGC 1065
           |||||||| |||| |||||||||||| |
Db      14 TATTTATTTATTATTTATTTATTTAAAC 41


RESULT 11
US-09-955-462A-2
; Sequence 2, Application US/09955462A
; Patent No. US20020150913A1
; GENERAL INFORMATION:
;  APPLICANT: Wilusz, Jeffrey
;  APPLICANT:  Wilusz, Carol
;  APPLICANT:  Gao, Min
;  TITLE OF INVENTION: Compositions and Methods for Reproducing and Modulating Mammal
;  TITLE OF INVENTION:  Messenger RNA Decapping
;  FILE REFERENCE: 601-1-109N
;  CURRENT APPLICATION NUMBER: US/09/955,462A
;  CURRENT FILING DATE:  2002-04-30
;  PRIOR APPLICATION NUMBER: US 60/233,682
;  PRIOR FILING DATE: 2000-09-19
;  NUMBER OF SEQ ID NOS: 3
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
;   LENGTH: 34
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: described in specification page 29
US-09-955-462A-2

  Query Match             1.2%;  Score 20.4;  DB 10;  Length 34;
  Best Local Similarity   23.3%;  Pred. No. 1.5e+05;
  Matches    7;  Conservative   17;  Mismatches    6;  Indels    0;  Gaps    0;

Qy   1029 TTATTAACCTATTTATTATTTATGTATTTA 1058
           ::  : |  :|:::|::|:::|: :|:::|
Db      5 UUUAUUAUUUAUUUAUUAUUUAUUUAUUUA 34


RESULT 12
US-09-864-785-3472
; Sequence 3472, Application US/09864785
; Patent No. US20020177568A1
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
;  APPLICANT:  Stinchcomb, Dan
;  APPLICANT:  Draper, Ken
;  APPLICANT:  McSwiggen, Jim
;  TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Rel
;  TITLE OF INVENTION:  Levels of NF-Kappa B
;  FILE REFERENCE: 400/022 (MBHB00-812-D)
;  CURRENT APPLICATION NUMBER: US/09/864,785
;  CURRENT FILING DATE:  2001-05-23
;  NUMBER OF SEQ ID NOS: 3929
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3472
;   LENGTH: 48
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Nucleic Acid
US-09-864-785-3472

  Query Match             1.2%;  Score 20.4;  DB 9;  Length 48;
  Best Local Similarity   60.9%;  Pred. No. 1.6e+05;
  Matches   28;  Conservative    2;  Mismatches   16;  Indels    0;  Gaps    0;

Qy     12 GAGACAGCAGAGCACACAAGCTTCTAGGACAAGAGCCAGGAAGAAA 57
          || || |  ||| | ||   |::| ||||||    || |||| |||
Db      1 GAUACUGAGGAGGAAACUCCCUUCAAGGACAUCGUCCGGGAAUAAA 46


RESULT 13
US-09-864-785-3568
```

```
; Sequence 3568, Application US/09864785
; Patent No. US20020177568A1
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
;  APPLICANT:  Stinchcomb, Dan
;  APPLICANT:  Draper, Ken
;  APPLICANT:  McSwiggen, Jim
;  TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relate
;  TITLE OF INVENTION:  Levels of NF-Kappa B
;  FILE REFERENCE: 400/022 (MBHB00-812-D)
;  CURRENT APPLICATION NUMBER: US/09/864,785
;  CURRENT FILING DATE:  2001-05-23
;  NUMBER OF SEQ ID NOS: 3929
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3568
;   LENGTH: 48
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Nucleic Acid
US-09-864-785-3568

  Query Match             1.2%;  Score 20.2;  DB 9;  Length 48;
  Best Local Similarity   63.4%;  Pred. No. 1.7e+05;
  Matches   26;  Conservative    2;  Mismatches   13;  Indels    0;  Gaps    0;

Qy      12 GAGACAGCAGAGCACACAAGCTTCTAGGACAAGAGCCAGGA 52
           |||| ||| ||| | ||   |::| ||||||    || |||
Db       1 GAGAGAGCGGAGGAAACUCCCUUCAAGGACAUCGUCCGGGA 41


RESULT 14
US-09-975-408-73/c
; Sequence 73, Application US/09975408
; Patent No. US20020150917A1
; GENERAL INFORMATION:
;  APPLICANT: Nanogen, Inc.
;  APPLICANT:  Weidenhammer, Elaine M.
;  APPLICANT:  Xu, Xiao
;  APPLICANT:  Kahl, Brenda F.
;  TITLE OF INVENTION: IMPROVED METHODS FOR GENE EXPRESSION MONITORING ON ELECTRONIC MIC
;  FILE REFERENCE: 267/174  Patrick S. Eagleman
;  CURRENT APPLICATION NUMBER: US/09/975,408
;  CURRENT FILING DATE:  2001-10-10
;  PRIOR APPLICATION NUMBER: 09/710,200
;  PRIOR FILING DATE: 2000-11-09
;  NUMBER OF SEQ ID NOS: 73
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 73
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: modified_base
;   LOCATION: (1)..(1)
;   OTHER INFORMATION: Biotinylated
US-09-975-408-73

  Query Match             1.2%;  Score 20;  DB 10;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+05;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     359 AGAAGTTTTTGAAGAGGGCT 378
           ||||||||||||||||||||
Db      20 AGAAGTTTTTGAAGAGGGCT 1


RESULT 15
US-10-075-579-73/c
; Sequence 73, Application US/10075579
; Patent No. US20020119484A1
; GENERAL INFORMATION:
;  APPLICANT: Nanogen, Inc.
;  APPLICANT:  Weidenhammer, Elaine M.
;  APPLICANT:  Wang, Ling
;  APPLICANT:  Xu, Xiao
;  APPLICANT:  Heller, Michael J.
;  APPLICANT:  Kahl, Brenda F.
;  TITLE OF INVENTION: IMPROVED METHODS FOR GENE EXPRESSION MONITORING ON ELECTRONIC
;  FILE REFERENCE: 256/262 Patrick S. Eagleman
;  CURRENT APPLICATION NUMBER: US/10/075,579
;  CURRENT FILING DATE:  2002-02-12
;  PRIOR APPLICATION NUMBER: US/09/710,200
;  PRIOR FILING DATE: 2000-11-09
;  NUMBER OF SEQ ID NOS: 73
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 73
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: modified_base
;   LOCATION: (1)..(1)
;   OTHER INFORMATION: Biotinylated
US-10-075-579-73

  Query Match             1.2%;  Score 20;  DB 12;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+05;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     359 AGAAGTTTTTGAAGAGGGCT 378
           ||||||||||||||||||||
Db      20 AGAAGTTTTTGAAGAGGGCT 1


RESULT 16
US-09-142-593-40/c
; Sequence 40, Application US/09142593
; Patent No. US20020016975A1
;  GENERAL INFORMATION:
;    APPLICANT:  HACKETT ET AL.
;    TITLE OF INVENTION:  DNA-BASED TRANSPOSON SYSTEM FOR THE
;    TITLE OF INVENTION:  INTRODUCTION OF NUCLEIC ACID INTO DNA OF A CELL
;    NUMBER OF SEQUENCES:  63
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  MUETING, RAASCH & GEBHARDT, P.A.
;      STREET:  119 NORTH FOURTH STREET, SUITE 203
;      CITY:  MINNEAPOLIS
;      STATE:  MINNESOTA
;      COUNTRY:  USA
;      ZIP:  55402
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/142,593
;      FILING DATE:  10-SEP-1998
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/040,664
;      FILING DATE:  11-MAR-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/053,868
;      FILING DATE:  28-JUL-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/065,303
;      FILING DATE:  13-NOV-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US98/04687
;      FILING DATE:  11-MAR-1998
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SANDBERG, VICTORIA A.
;      REGISTRATION NUMBER:  41,287
;      REFERENCE/DOCKET NUMBER:  110.00450101
```

```
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  612-305-1226
;      TELEFAX:  612-305-1228
;  INFORMATION FOR SEQ ID NO:  40:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  28 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-09-142-593-40

  Query Match             1.2%;  Score 20;  DB 10;  Length 28;
  Best Local Similarity   82.1%;  Pred. No. 1.7e+05;
  Matches   23;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy      75 CTCACTGTGTGTAAACATGACTTCCAAG 102
           || | ||| ||||||| |||||| ||||
Db      28 CTTATTGTATGTAAACTTGACTTTCAAG 1


RESULT 17
US-09-864-785-3460
; Sequence 3460, Application US/09864785
; Patent No. US20020177568A1
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
;  APPLICANT:  Stinchcomb, Dan
;  APPLICANT:  Draper, Ken
;  APPLICANT:  McSwiggen, Jim
;  TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relate
;  TITLE OF INVENTION:  Levels of NF-Kappa B
;  FILE REFERENCE: 400/022 (MBHB00-812-D)
;  CURRENT APPLICATION NUMBER: US/09/864,785
;  CURRENT FILING DATE:  2001-05-23
;  NUMBER OF SEQ ID NOS: 3929
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3460
;   LENGTH: 48
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Nucleic Acid
US-09-864-785-3460

  Query Match             1.2%;  Score 20;  DB 9;  Length 48;
  Best Local Similarity   61.4%;  Pred. No. 1.9e+05;
  Matches   27;  Conservative    2;  Mismatches   15;  Indels    0;  Gaps    0;

Qy      13 AGACAGCAGAGCACACAAGCTTCTAGGACAAGAGCCAGGAAGAA 56
           ||||| | ||| | ||   |::| ||||||    || |||  ||
Db       2 AGACAUCGGAGGAAACUCCCUUCAAGGACAUCGUCCGGGACAAA 45


RESULT 18
US-09-828-523A-96
; Sequence 96, Application US/09828523A
; Patent No. US20020168697A1
; GENERAL INFORMATION:
;  APPLICANT: The Pharmacia & Upjohn Company
;  TITLE OF INVENTION: ANTIMICROBIAL METHODS AND MATERIALS
;  FILE REFERENCE: 268.62120101
;  CURRENT APPLICATION NUMBER: US/09/828,523A
;  CURRENT FILING DATE:  2001-04-06
;  PRIOR APPLICATION NUMBER: 60/266,327
;  PRIOR FILING DATE: 2000-04-06
;  NUMBER OF SEQ ID NOS: 99
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 96
;   LENGTH: 43
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Oligonucleotide Primer.
US-09-828-523A-96

  Query Match             1.2%;  Score 19.8;  DB 9;  Length 43;
  Best Local Similarity   69.2%;  Pred. No. 2e+05;
  Matches   27;  Conservative    0;  Mismatches   12;  Indels    0;  Gaps    0;

Qy     612 ATCTACAAAAAACAACAAATAATTTTTGAATATAAGGAT 650
           |||| |||| || | |   |||||||  |||  ||| ||
Db       4 ATCTGCAAATAATATCTTTTAATTTTAAAATTAAAGAAT 42


RESULT 19
US-09-825-805-64
; Sequence 64, Application US/09825805
; Publication No. US20030004122A1
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
;  APPLICANT:  Beigelman, Leo
;  APPLICANT:  Beaudry, Amber
;  APPLICANT:  Karpeisky, Alex
;  APPLICANT:  Adamic, Jasenka Matulic
;  APPLICANT:  Sweedler, Dave
;  APPLICANT:  Zinnen, Shawn
;  TITLE OF INVENTION: Nucleotide Triphosphate and their Incorporation into Oligonucl
;  FILE REFERENCE: MBHB00-831-F (400/009)
;  CURRENT APPLICATION NUMBER: US/09/825,805
;  CURRENT FILING DATE:  2001-09-27
;  PRIOR APPLICATION NUMBER: 09/578,223
;  PRIOR FILING DATE: 2000-05-23
;  PRIOR APPLICATION NUMBER: 09/476,387
;  PRIOR FILING DATE: 1999-12-30
;  PRIOR APPLICATION NUMBER: 09/474,432
;  PRIOR FILING DATE: 1999-12-29
;  PRIOR APPLICATION NUMBER: 09/301,511
;  PRIOR FILING DATE: 1999-04-28
;  PRIOR APPLICATION NUMBER: 09/186,675
;  PRIOR FILING DATE: 1998-11-04
;  PRIOR APPLICATION NUMBER: 60/083,727
;  PRIOR FILING DATE: 1998-04-29
;  PRIOR APPLICATION NUMBER: 60/064,866
;  PRIOR FILING DATE: 1997-11-05
;  NUMBER OF SEQ ID NOS: 1558
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 64
;   LENGTH: 48
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Enzymatic Nucleic Acid
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(10)
;   OTHER INFORMATION: 2'-O-Methyl
;   NAME/KEY: misc_feature
;   LOCATION: (12)..(21)
;   OTHER INFORMATION: 2'-O-Methyl
;   NAME/KEY: misc_feature
;   LOCATION: (43)..(47)
;   OTHER INFORMATION: 2'-O-Methyl
;   NAME/KEY: misc_feature
;   LOCATION: (22)..(26)
;   OTHER INFORMATION: 2'-deoxy-2'-amino
;   NAME/KEY: misc_feature
;   LOCATION: (32)..(32)
;   OTHER INFORMATION: 2'-deoxy-2'-amino
;   NAME/KEY: misc_feature
;   LOCATION: (34)..(35)
;   OTHER INFORMATION: 2'-deoxy-2'-amino
;   NAME/KEY: misc_feature
;   LOCATION: (37)..(39)
;   OTHER INFORMATION: 2'-deoxy-2'-amino
;   NAME/KEY: misc_feature
;   LOCATION: (48)..(48)
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; OTHER INFORMATION: n stands for inverted deoxyabasic derivative
US-09-825-805-64

  Query Match 1.2%; Score 19.8; DB 9; Length 48;
  Best Local Similarity 59.6%; Pred. No. 2e+05;
  Matches 28; Conservative 2; Mismatches 17; Indels 0; Gaps 0;

Qy 10 CAGAGACAGCAGAGCACACAAGCTTCTAGGACAAGAGCCAGGAAGAA 56
Db 1 CGGGGUUAUCGGAGGAAACUCCCUUCAAGGACAUCGUCCGGGAAGAA 47

RESULT 20
US-10-017-736-9/c
; Sequence 9, Application US/10017736
; Publication No. US20020192640A1
; GENERAL INFORMATION:
; APPLICANT: Boehringer Ingelheim (Canada) Ltd.
; TITLE OF INVENTION: Purified Active HCV NS2/3 Protease
; FILE REFERENCE: 13/082
; CURRENT APPLICATION NUMBER: US/10/017,736
; CURRENT FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: 60/256,031
; PRIOR FILING DATE: 2000-12-15
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 45
; TYPE: DNA
; ORGANISM: HCV
US-10-017-736-9

  Query Match 1.2%; Score 19.6; DB 9; Length 45;
  Best Local Similarity 66.7%; Pred. No. 2.2e+05;
  Matches 28; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

Qy 813 ATTTAGCTGGAAATCCTGGATTTTTTTCTGTTAAATCTGGCA 854
Db 45 ATGGTGATGGTGATGCTCGAGCTTTTTCTTTTTCATATGGCA 4

Search completed: February 9, 2003, 19:24:29
Job time : 136 secs

GenCore version 5.1.3

OM nucleic - nucleic search, using sw model

Run on: February 9, 2003, 17:18:47 ; Search time 2362 Seconds
(without alignments)
11238.104 Million cell updates/sec

Title: US-09-960-143-3
Perfect score: 1639
Sequence: 1 acaaactttcagagacagca.....atataatttgttgtcaaagt 1639

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 102860

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	23.8	1.5	43	17	AZ404728	AZ404728 1M0173I08
	2	23.2	1.4	46	13	BJ015738	BJ015738 BJ015738
c	3	23	1.4	50	12	BF029726	BF029726 601556615
c	4	22.8	1.4	46	14	BQ704909	BQ704909 Bn01_01c2
	5	22.8	1.4	49	13	BJ054665	BJ054665 BJ054665
c	6	22.8	1.4	49	17	AZ333209	AZ333209 1M0062L10
	7	22.6	1.4	46	9	AU009443	AU009443 AU009443
	8	22.6	1.4	46	9	AU009444	AU009444 AU009444
	9	22.4	1.4	48	9	AU266602	AU266602 AU266602
	10	22.4	1.4	48	17	TA26E09Q	AL452944 T. brucei
c	11	22.4	1.4	49	17	AZ346760	AZ346760 1M0082F12
	12	22.4	1.4	50	10	AW333744	AW333744 S25E9 AGS
	13	22.2	1.4	40	17	AZ615013	AZ615013 1M0444C09
	14	22.2	1.4	48	13	BJ078372	BJ078372 BJ078372
	15	22	1.3	50	9	AU268417	AU268417 AU268417
	16	21.6	1.3	49	12	BG179823	BG179823 602329028
c	17	21.6	1.3	49	13	BI745472	BI745472 rk81a10.y
c	18	21.6	1.3	50	10	AV957350	AV957350 AV957350
	19	21.4	1.3	44	17	BH853222	BH853222 SALK_0762
	20	21.4	1.3	45	17	BH850240	BH850240 SALK_0710
	21	21.4	1.3	47	17	TA48H05P	AL457070 T. brucei
	22	21.2	1.3	34	13	BJ052720	BJ052720 BJ052720
	23	21.2	1.3	43	17	AZ586882	AZ586882 1M0394F11
	24	21.2	1.3	45	9	AU267061	AU267061 AU267061
	25	21.2	1.3	45	17	BH789466	BH789466 SALK_0296
	26	21.2	1.3	45	17	BH799966	BH799966 1008110H1
c	27	21.2	1.3	45	17	TA344F02P	AL493895 T. brucei
c	28	21.2	1.3	50	17	BH861292	BH861292 SALK_0679
c	29	21.2	1.3	50	17	TA187C12P	AL477525 T. brucei
	30	21	1.3	39	9	AU267631	AU267631 AU267631
c	31	21	1.3	43	14	T25548	T25548 EST00581 Un
	32	21	1.3	47	9	AU265820	AU265820 AU265820
	33	21	1.3	48	13	BJ083775	BJ083775 BJ083775
	34	21	1.3	50	9	AU006647	AU006647 AU006647
	35	21	1.3	50	17	AZ950287	AZ950287 2M0214K17
c	36	20.8	1.3	39	9	AU266450	AU266450 AU266450
c	37	20.8	1.3	44	10	AV834222	AV834222 AV834222
c	38	20.8	1.3	45	14	D34826	D34826 CELK013AYF
c	39	20.8	1.3	48	9	AU263470	AU263470 AU263470
c	40	20.8	1.3	48	12	BG667239	BG667239 DRABDB04
c	41	20.8	1.3	48	14	C21451	C21451 HUMGS001043
	42	20.8	1.3	49	13	BI863578	BI863578 kx45h10.y
c	43	20.6	1.3	45	17	BH792269	BH792269 SALK_0632
c	44	20.6	1.3	49	13	BI863578	BI863578 kx45h10.y
	45	20.6	1.3	50	13	BM126011	BM126011 if04c10.x

ALIGNMENTS

RESULT 1
AZ404728
LOCUS AZ404728 43 bp DNA linear GSS 03-OCT-2000
DEFINITION 1M0173I08F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0173I08 F, DNA sequence.
ACCESSION AZ404728
VERSION AZ404728.1 GI:10528741
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 43)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00

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           Plate: 0173  row: I  column: 08
           Seq primer: CGTTGTAAAACGACGGCCAGT
           Class: plasmid ends
           High quality sequence stop: 43.
FEATURES             Location/Qualifiers
     source          1. .43
                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0173I08"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
BASE COUNT       12 a      4 c      2 g     25 t
ORIGIN

  Query Match             1.5%;  Score 23.8;  DB 17;  Length 43;
  Best Local Similarity   92.6%;  Pred. No. 2.1e+06;
  Matches   25;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy    1036 CCTATTTATTATTTATGTATTTATTTA 1062
           ||||||||||| ||||| ||||||||||
Db       1 CCTATTTATTTTTTATTTATTTATTTA 27


RESULT 2
BJ015738
LOCUS       BJ015738                  46 bp    mRNA    linear   EST 07-DEC-2001
DEFINITION  BJ015738 MF01SSA cDNA Oryzias latipes cDNA clone MF01SSA003D06 3',
            mRNA sequence.
ACCESSION   BJ015738
VERSION     BJ015738.1  GI:17410289
KEYWORDS    EST.
SOURCE      Japanese medaka.
  ORGANISM  Oryzias latipes
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
            Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
            Beloniformes; Adrianichthyidae; Oryziinae; Oryzias.
REFERENCE   1  (bases 1 to 46)
  AUTHORS   Kohara,Y., Shin-i,T., Kimura,T., Narita,T., Jindo,T. and Takeda,H.
  TITLE     Medaka EST Project in Takeda's lab
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Tadasu Shin-i
            Center For Genetic Resource Information
            National Institute of Genetics
            1111 Yata, Mishima, Shizuoka 411-8540, Japan
            Tel: 81-559-81-6856
            Fax: 81-559-81-6855
            Email: tshini@genes.nig.ac.jp.
FEATURES             Location/Qualifiers
     source          1. .46
                     /organism="Oryzias latipes"
                     /strain="Hd-rR"
                     /db_xref="taxon:8090"
                     /clone="MF01SSA003D06"
                     /clone_lib="MF01SSA cDNA"
                     /sex="mixture of female and male"
                     /tissue_type="whole embryo"
                     /dev_stage="segmentation stage 20 - 25"
BASE COUNT       32 a      0 c      6 g      7 t      1 others
ORIGIN

  Query Match             1.4%;  Score 23.2;  DB 13;  Length 46;
  Best Local Similarity   68.9%;  Pred. No. 2.6e+06;
  Matches   31;  Conservative    0;  Mismatches   14;  Indels    0;  Gaps    0;

Qy    1582 TTGTATGGAAATATAAAAGTAAATATGAAACATTTAAAATATAAT 1626
           |||   ||||| | ||||  ||| |  |||  ||||||| | |||
Db       1 TTGGGGGGAAAAAAAAAAAAAAAAAAAAATNTTTAAAAAAAAAT 45


RESULT 3
BF029726/c
LOCUS       BF029726                  50 bp    mRNA    linear   EST 10-OCT-2000
DEFINITION  601556615F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3826730 5',
            mRNA sequence.
ACCESSION   BF029726
VERSION     BF029726.1  GI:10737438
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 50)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
             cDNA Library Preparation: CLONETECH Laboratories, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM494  row: m  column: 03.
FEATURES             Location/Qualifiers
     source          1. .50
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:3826730"
                     /clone_lib="NIH_MGC_58"
                     /tissue_type="hypernephroma"
                     /lab_host="DH10B (T1 phage-resistant)"
                     /note="Organ: kidney; Vector: pDNR-LIB (Clontech); Site_1:
                     SfiI (ggccgcctcggcc); Site_2: SfiI (ggccattatggcc);
                     Double-stranded cDNA was prepared from cell line RNA.  5'
                     and 3' adaptors were used in cloning as follows: 5'
                     adaptor sequence:  5'-CACGGCCATTATGGCC-3' and 3' adaptor
                     sequence:  5'-ATTCTAGAGGCCGAGGCGGCCGACATG-dT(30)BN-3'
                     (where B = A, C, or G and N = A, C,  G, or T).   Average
                     insert size 1.35 kb (range 0.9-4.0 kb).  15/15 colonies
                     contained  inserts by PCR. This library was enriched for
                     full-length clones and was constructed by Clontech
                     Laboratories (Palo Alto, CA)."
BASE COUNT       42 a      0 c      3 g      5 t
ORIGIN

  Query Match             1.4%;  Score 23;  DB 12;  Length 50;
  Best Local Similarity   68.1%;  Pred. No. 2.8e+06;
  Matches   32;  Conservative    0;  Mismatches   15;  Indels    0;  Gaps    0;

Qy    1015 TTTTCAAGTGTAACTTATTAACCTATTTATTATTTATGTATTTATTT 1061
           |||| |  | ||| || |||  || ||| || ||| | | ||| |||
Db      48 TTTTTATTTCTAATTTTTTATTCTTTTTTTTTTTTTTATTTTTTTTT 2
```

```
RESULT 4
BQ704909/c
LOCUS       BQ704909                 46 bp    mRNA    linear   EST 16-JUL-2002
DEFINITION  Bn01_01c23_A
            Bn01_AAFC_ECORC_transgenic_Brassica_napus_overexpressing_BNCBF17_co
            nstitutively_frost_tolerant Brassica napus cDNA clone Bn01_01c23,
            mRNA sequence.
ACCESSION   BQ704909
VERSION     BQ704909.1  GI:21844328
KEYWORDS    EST.
SOURCE      rape.
  ORGANISM  Brassica napus
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE   1  (bases 1 to 46)
  AUTHORS   Singh,J., Allard,G., Tinker,N., Robert,L., Lacroix,C., De Moors,A.,
            Chagnon,J., Farah,S., Couroux,P. and Hattori,J.
  TITLE     Expressed Sequence Tags from constitutively frost tolerant
            transgenic Brassica napus overexpressing BNCBF17
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Singh,J.A.
            Eastern Cereal and Oilseed Research Centre
            Agriculture and Agri-food Canada
            KW Neatby Bldg., Central Experimental Farm, Ottawa, Ontario, K1A
            0C6, Canada
            Tel: (613) 759-1662
            Fax: (613) 759-1701
            Email: singhja@em.agr.ca.
FEATURES             Location/Qualifiers
     source          1. .46
                     /organism="Brassica napus"
                     /cultivar="Westar"
                     /db_xref="taxon:3708"
                     /clone="Bn01_01c23"
                     /clone_lib="Bn01_AAFC_ECORC_transgenic_Brassica_napus_over
                     expressing_BNCBF17_constitutively_frost_tolerant"
                     /tissue_type="fourth leaf"
                     /dev_stage="3 weeks seedling grown at room temperature"
                     /note="Vector: Bluescript SK+/XhoI-EcoRI; Site_1: EcoRI;
                     Site_2: XhoI; Germinated in soil flats and seedlings grown
                     for 3 weeks in a Conviron E-15 cabinet set at 20oC /16 hr
                     light (250 Em-2sec-1) and 16 oC / 8 hr dark. Fourth leaves
                     collected at 9 am and immediately frozen."
BASE COUNT       11 a      9 c      4 g     22 t
ORIGIN

  Query Match             1.4%;  Score 22.8;  DB 14;  Length 46;
  Best Local Similarity   79.4%;  Pred. No. 3.1e+06;
  Matches   27;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy     597 GTATTATTTATTTGAATCTACAAAAAACAACAAA 630
           || || ||| |||||| | | |||||| ||||||
Db      36 GTCTTGTTTGTTTGAAACAAAAAAAAAAACAAA 3


RESULT 5
BJ054665
LOCUS       BJ054665                 49 bp    mRNA    linear   EST 07-DEC-2001
DEFINITION  BJ054665 NIBB Mochii normalized Xenopus neurula library Xenopus
            laevis cDNA clone XL044p13 3', mRNA sequence.
ACCESSION   BJ054665
VERSION     BJ054665.1  GI:17422989
KEYWORDS    EST.
SOURCE      African clawed frog.
  ORGANISM  Xenopus laevis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
            Xenopodinae; Xenopus.
REFERENCE   1  (bases 1 to 49)
  AUTHORS   Kitayama,A., Terasaka,C., Mochii,M., Ueno,N., Shin-i,T. and Kohara
            ,Y.
  TITLE     Expressed genes in X. laevis embryo
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Tadasu Shin-i
            Center For Genetic Resource Information
            National Institute of Genetics
            1111 Yata, Mishima, Shizuoka 411-8540, Japan
            Tel: 81-559-81-6856
            Fax: 81-559-81-6855
            Email: tshini@genes.nig.ac.jp.
FEATURES             Location/Qualifiers
     source          1. .49
                     /organism="Xenopus laevis"
                     /db_xref="taxon:8355"
                     /clone="XL044p13"
                     /clone_lib="NIBB Mochii normalized Xenopus neurula
                     library"
                     /tissue_type="whole embryo"
                     /dev_stage="stage 15"
                     /note="Vector: pBSRN3; Site_1: NotI; Site_2: EcoRI; cDNAs
                     were oligo-dT primed and directionally cloned. Staging
                     according to  Nieuwkoop and Faber. Library is subtracted
                     and was constructed by N. Garrett  and A.M. Zorn,
                     (Wellcome/CRC Institute). "
BASE COUNT       21 a      4 c      9 g     14 t      1 others
ORIGIN

  Query Match             1.4%;  Score 22.8;  DB 13;  Length 49;
  Best Local Similarity   69.8%;  Pred. No. 3.1e+06;
  Matches   30;  Conservative    0;  Mismatches   13;  Indels    0;  Gaps    0;

Qy    1580 GATTGTATGGAAATATAAAAGTAAATATGAAACATTTAAAATA 1622
           ||  ||    ||| |||||||| | |||  |||| ||| ||||
Db       6 GAGGGTNCTTAAAAATAAAAGTCATTATCTAACAGTTATAATA 48


RESULT 6
AZ333209/c
LOCUS       AZ333209                 49 bp    DNA     linear   GSS 29-SEP-2000
DEFINITION  1M0062L10F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0062L10 F, DNA sequence.
ACCESSION   AZ333209
VERSION     AZ333209.1  GI:10397601
KEYWORDS    GSS.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 49)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
            ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
            and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0062  row: L  column: 10
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 49.
FEATURES             Location/Qualifiers
     source          1. .49
                     /organism="Mus musculus"
                     /strain="C57BL/6J"
```

```
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0062L10"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
BASE COUNT       24 a      0 c      0 g     25 t
ORIGIN

  Query Match             1.4%;  Score 22.8;  DB 17;  Length 49;
  Best Local Similarity   71.4%;  Pred. No. 3.1e+06;
  Matches   30;  Conservative    0;  Mismatches   12;  Indels    0;  Gaps    0;

Qy   1139 TAAATTTATTTTATTTTAGATATTAAATGATGTTTTATTAGA 1180
           ||| | |||| |||  || |||||| || ||  | ||||| |
Db     43 TAATTATATTATATAATATATTATTATATAATAATATATTATA 2


RESULT 7
AU009443
LOCUS       AU009443                 46 bp    mRNA    linear   EST 31-JUL-1998
DEFINITION  AU009443 Schizosaccharomyces pombe late log phase cDNA
            Schizosaccharomyces pombe cDNA clone spc04922, mRNA sequence.
ACCESSION   AU009443
VERSION     AU009443.1  GI:3346123
KEYWORDS    EST.
SOURCE      fission yeast.
  ORGANISM  Schizosaccharomyces pombe
            Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
            Schizosaccharomycetales; Schizosaccharomycetaceae;
            Schizosaccharomyces.
REFERENCE   1  (bases 1 to 46)
  AUTHORS   Morimyo,M. and Mita,K.
  TITLE     Identification of expressed sequence tags of Schizosaccharomyces
            pombe
  JOURNAL   Unpublished (1998)
COMMENT     Contact: Mitsuoki Morimyo
            Genome Research Group
            National Institute of Radiological Sciences
            9-1, Anagawa-4-chome, Inage-ku, Chiba, Chiba 263-8555, Japan
            Email: morimyo@nirs.go.jp.
FEATURES             Location/Qualifiers
     source          1. .46
                     /organism="Schizosaccharomyces pombe"
                     /strain="972"
                     /db_xref="taxon:4896"
                     /clone="spc04922"
                     /clone_lib="Schizosaccharomyces pombe late log phase cDNA"
                     /sex="h minus"
                     /note="Vector: M13mp19; The cDNA library of
                     Schizosaccharomyces pombe was prepared by cloning cDNA
                     into the SmaI site of M13mp19 DNA and the direction of DNA
                     sequences was not always from 5' to 3'. The cDNA data of
                     Schizosaccharomyces pombe are available for searching on
                     the World Wide Web.  (URL, http://www.nirs.go.jp)"
BASE COUNT       27 a      2 c      3 g     14 t
ORIGIN

  Query Match             1.4%;  Score 22.6;  DB 9;  Length 46;
  Best Local Similarity   68.9%;  Pred. No. 3.4e+06;
  Matches   31;  Conservative    0;  Mismatches   14;  Indels    0;  Gaps    0;

Qy    582 ATACTTATATGTAAAGTATTATTTATTTGAATCTACAAAAAACAA 626
          | | |||||  |||| |    |  |||||||  |||||||| ||
Db      2 AAAATTATACTTAAAATTAATTAAATTTGAATTGACAAAAAAAAA 46


RESULT 8
AU009444
LOCUS       AU009444                 46 bp    mRNA    linear   EST 31-JUL-1998
DEFINITION  AU009444 Schizosaccharomyces pombe late log phase cDNA
            Schizosaccharomyces pombe cDNA clone spc04923, mRNA sequence.
ACCESSION   AU009444
VERSION     AU009444.1  GI:3346124
KEYWORDS    EST.
SOURCE      fission yeast.
  ORGANISM  Schizosaccharomyces pombe
            Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
            Schizosaccharomycetales; Schizosaccharomycetaceae;
            Schizosaccharomyces.
REFERENCE   1  (bases 1 to 46)
  AUTHORS   Morimyo,M. and Mita,K.
  TITLE     Identification of expressed sequence tags of Schizosaccharomyces
            pombe
  JOURNAL   Unpublished (1998)
COMMENT     Contact: Mitsuoki Morimyo
            Genome Research Group
            National Institute of Radiological Sciences
            9-1, Anagawa-4-chome, Inage-ku, Chiba, Chiba 263-8555, Japan
            Email: morimyo@nirs.go.jp.
FEATURES             Location/Qualifiers
     source          1. .46
                     /organism="Schizosaccharomyces pombe"
                     /strain="972"
                     /db_xref="taxon:4896"
                     /clone="spc04923"
                     /clone_lib="Schizosaccharomyces pombe late log phase cDNA"
                     /sex="h minus"
                     /note="Vector: M13mp19; The cDNA library of
                     Schizosaccharomyces pombe was prepared by cloning cDNA
                     into the SmaI site of M13mp19 DNA and the direction of DNA
                     sequences was not always from 5' to 3'. The cDNA data of
                     Schizosaccharomyces pombe are available for searching on
                     the World Wide Web.  (URL, http://www.nirs.go.jp)"
BASE COUNT       27 a      2 c      3 g     14 t
ORIGIN

  Query Match             1.4%;  Score 22.6;  DB 9;  Length 46;
  Best Local Similarity   68.9%;  Pred. No. 3.4e+06;
  Matches   31;  Conservative    0;  Mismatches   14;  Indels    0;  Gaps    0;

Qy    582 ATACTTATATGTAAAGTATTATTTATTTGAATCTACAAAAAACAA 626
          | | |||||  |||| |    |  |||||||  |||||||| ||
Db      2 AAAATTATACTTAAAATTAATTAAATTTGAATTGACAAAAAAAAA 46


RESULT 9
AU266602
LOCUS       AU266602                 48 bp    mRNA    linear   EST 10-MAY-2002
DEFINITION  AU266602 VS Dictyostelium discoideum cDNA clone VSG534 5', mRNA
            sequence.
ACCESSION   AU266602
VERSION     AU266602.1  GI:20525400
KEYWORDS    EST.
SOURCE      Dictyostelium discoideum.
  ORGANISM  Dictyostelium discoideum
            Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
REFERENCE   1  (bases 1 to 48)
```

```
  AUTHORS   Urushihara,H., Morio,T., Saito,T., Koriki,E., Ochiai,H., Maeda,M.,
            Takeuchi,I., Kohara,Y. and Tanaka,Y.
  TITLE     Population analysis of cDNAs from unicellular and multicellular
            stages of Dictyostelium discoideum
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Hideko Urushihara
            Institute of Biological Sciences
            University of Tsukuba
            1-1-1 Tennoudai, Tsukuba, Ibaraki 305-8572, Japan
            Tel: 81-298-53-4664
            Fax: 81-298-53-6614
            Email: hideko@biol.tsukuba.ac.jp.
FEATURES             Location/Qualifiers
     source          1. .48
                     /organism="Dictyostelium discoideum"
                     /strain="AX4"
                     /db_xref="taxon:44689"
                     /clone="VSG534"
                     /clone_lib="VS"
                     /sex="mat A"
                     /dev_stage="vegetative"
BASE COUNT       30 a      3 c      1 g     14 t
ORIGIN

  Query Match             1.4%;  Score 22.4;  DB 9;  Length 48;
  Best Local Similarity   66.7%;  Pred. No. 3.6e+06;
  Matches   32;  Conservative    0;  Mismatches   16;  Indels    0;  Gaps    0;

Qy     576 CAGAACATACTTATATGTAAAGTATTATTTATTTGAATCTACAAAAAA 623
           | ||| | ||  |||  |||| ||  |||| |||  ||  | ||||||
Db       1 CCGAAAAAACAAATAAATAAATTAAAATTTTTTTTTATAAAAAAAAAA 48


RESULT 10
TA26E09Q
LOCUS       TA26E09Q                  48 bp    DNA     linear   GSS 13-DEC-2000
DEFINITION  T. brucei sheared genomic DNA clone 26e09, reverse sequence,
            genomic survey sequence.
ACCESSION   AL452944
VERSION     AL452944.1  GI:11850929
KEYWORDS    GSS.
SOURCE      Trypanosoma brucei.
  ORGANISM  Trypanosoma brucei
            Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
            Trypanosoma.
REFERENCE   1  (bases 1 to 48)
  AUTHORS   Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,
            Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,
            Melville,S.E., Rajandream,M.A. and Barrell,B.G.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
            project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
            Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
            nhl@sanger.ac.uk
COMMENT     Constructed at the Institute for Genomic Research (TIGR),
            Rockville, MD. Genomic DNA isolated from a cloned population of
            Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
            to give a tight size distribution (
            4 kb).  The v + i method used for the library construction is
            described in detail in Smith, H. and Venter, J.C. (Making small
            insert libraries for whole genome shotgun sequencing projects.  In
            Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
            Barrell, Oxford University Press, 1999).
            Email: nelsayed@tigr.org
            Details of T. brucei sequencing at the Sanger Centre are available
            at http://www.sanger.ac.uk/Projects/T_brucei/.
FEATURES             Location/Qualifiers
     source          1. .48
                     /organism="Trypanosoma brucei"
                     /strain="TREU927"
                     /db_xref="taxon:5691"
                     /clone="26e09"
BASE COUNT       18 a      7 c      8 g     15 t
ORIGIN

  Query Match             1.4%;  Score 22.4;  DB 17;  Length 48;
  Best Local Similarity   72.5%;  Pred. No. 3.6e+06;
  Matches   29;  Conservative    0;  Mismatches   11;  Indels    0;  Gaps    0;

Qy    1485 ATATTATTTAAATGACTGCATTTTTAAATACAAGGCTTTA 1524
           |||||| ||| | |  ||||   ||||||||||  | ||
Db       7 ATATTAATTACAAGTGTGCAACATTAAATACAAGTGTGTA 46


RESULT 11
AZ346760/c
LOCUS       AZ346760                  49 bp    DNA     linear   GSS 29-SEP-2000
DEFINITION  1M0082F12F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0082F12 F, DNA sequence.
ACCESSION   AZ346760
VERSION     AZ346760.1  GI:10425997
KEYWORDS    GSS.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 49)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
            ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
            and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0082  row: F  column: 12
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 49.
FEATURES             Location/Qualifiers
     source          1. .49
                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0082F12"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
BASE COUNT       39 a      4 c      0 g      6 t
```

```
ORIGIN

  Query Match             1.4%;  Score 22.4;  DB 17;  Length 49;
  Best Local Similarity   66.7%;  Pred. No. 3.6e+06;
  Matches   32;  Conservative    0;  Mismatches   16;  Indels    0;  Gaps    0;

Qy   1014 ATTTTCAAGTGTAACTTATTAACCTATTTATTATTTATGTATTTATTT 1061
          ||| |   || |   || |||   |||||||||||||| | | | |||
Db     49 ATTGTTTTGTTTTGTTTTTTATTTTATTTATTATTTATTTTTGTTTTT 2


RESULT 12
AW333744
LOCUS       AW333744                 50 bp    mRNA    linear   EST 31-JAN-2000
DEFINITION  S25E9 AGS-1 Pneumocystis carinii f. sp. carinii cDNA 3', mRNA
            sequence.
ACCESSION   AW333744
VERSION     AW333744.1  GI:6830101
KEYWORDS    EST.
SOURCE      Pneumocystis carinii f. sp. carinii.
  ORGANISM  Pneumocystis carinii f. sp. carinii
            Eukaryota; Fungi; Ascomycota; Pneumocystidomycetes;
            Pneumocystidaceae; Pneumocystis.
REFERENCE   1  (bases 1 to 50)
  AUTHORS   Smulian,A.G., Arnold,J., Weise,M., Wunderlich,J., Staben,C., Edman
            ,J.C., Kovacs,J. and Cushion,M.
  TITLE     Expressed sequence tags from Pneumocystis carinii
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Staben C
            School of Biological Sciences
            University of Kentucky
            101 Morgan Building, University of Kentucky, Lexington, KY
            40506-0225, USA
            Tel: 606 257 2161
            Fax: 606 257 1717
            Email: staben@pop.uky.edu.
FEATURES             Location/Qualifiers
     source          1. .50
                     /organism="Pneumocystis carinii f. sp. carinii"
                     /db_xref="taxon:38081"
                     /clone_lib="AGS-1"
                     /lab_host="E. coli"
                     /note="Vector: Lambda ZAP II; Site_1: EcoRI; Site_2: XhoI;
                     P. carinii organisms (3x10e9) from a single rat (99-1-6,
                     sacrificed on 3/17/99)  at Cincinnati VA facilities.
                     Trizol extracted RNA.  Oligo dT priming, standard
                     conditions described by  vendor, Stratagene. Further
                     details see www.uky.edu/Project/Pneumocystis/"
BASE COUNT       21 a      1 c      1 g     27 t
ORIGIN

  Query Match             1.4%;  Score 22.4;  DB 10;  Length 50;
  Best Local Similarity   66.7%;  Pred. No. 3.6e+06;
  Matches   32;  Conservative    0;  Mismatches   16;  Indels    0;  Gaps    0;

Qy   1143 TTTATTTTATTTTAGATATTAAATGATGTTTTATTAGATAAATTTCAA 1190
          ||| |||| ||||   ||  ||||||     ||||| ||  |||| ||
Db      2 TTTTTTTTTTTTTTTTTAAAAAATGAAAAAATATTAAATCTATTTAAA 49


RESULT 13
AZ615013
LOCUS       AZ615013                 40 bp    DNA     linear   GSS 13-DEC-2000
DEFINITION  1M0444C09F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0444C09 F, DNA sequence.
ACCESSION   AZ615013
VERSION     AZ615013.1  GI:11737203
KEYWORDS    GSS.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 40)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
            ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
            and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0444  row: C  column: 09
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 40.
FEATURES             Location/Qualifiers
     source          1. .40
                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0444C09"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
BASE COUNT       13 a      0 c      1 g     26 t
ORIGIN

  Query Match             1.4%;  Score 22.2;  DB 17;  Length 40;
  Best Local Similarity   77.1%;  Pred. No. 4.1e+06;
  Matches   27;  Conservative    0;  Mismatches    8;  Indels    0;  Gaps    0;

Qy   1044 TTATTTATGTATTTATTTAAGCATCAAATATTTGT 1078
          |||||||| |||||||||   ||  | ||| |||
Db      3 TTATTTATTTATTTATTTATTTATTTATTATATGT 37


RESULT 14
BJ078372
LOCUS       BJ078372                 48 bp    mRNA    linear   EST 11-DEC-2001
DEFINITION  BJ078372 NIBB Mochii normalized Xenopus tailbud library Xenopus
            laevis cDNA clone XL063p03 3', mRNA sequence.
ACCESSION   BJ078372
VERSION     BJ078372.1  GI:17523288
KEYWORDS    EST.
SOURCE      African clawed frog.
  ORGANISM  Xenopus laevis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
            Xenopodinae; Xenopus.
```

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REFERENCE   1  (bases 1 to 48)
  AUTHORS   Kitayama,A., Terasaka,C., Mochii,M., Ueno,N., Shin-i,T. and Kohara
            ,Y.
  TITLE     Expressed genes in X. laevis embryo
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Tadasu Shin-i
            Center For Genetic Resource Information
            National Institute of Genetics
            1111 Yata, Mishima, Shizuoka 411-8540, Japan
            Tel: 81-559-81-6856
            Fax: 81-559-81-6855
            Email: tshini@genes.nig.ac.jp.
FEATURES             Location/Qualifiers
     source          1. .48
                     /organism="Xenopus laevis"
                     /db_xref="taxon:8355"
                     /clone="XL063p03"
                     /clone_lib="NIBB Mochii normalized Xenopus tailbud
                     library"
                     /tissue_type="whole embryo"
                     /dev_stage="stage 25"
                     /note="Vector: pBSRN3; Site_1: NotI; Site_2: EcoRI; cDNAs
                     were oligo-dT primed and directionally cloned. Staging
                     according to  Nieuwkoop and Faber. Library is subtracted
                     and was constructed by N. Garrett  and A.M. Zorn,
                     (Wellcome/CRC Institute). "
BASE COUNT       24 a      6 c      5 g     13 t
ORIGIN

  Query Match             1.4%;  Score 22.2;  DB 13;  Length 48;
  Best Local Similarity   77.1%;  Pred. No. 3.9e+06;
  Matches   27;  Conservative    0;  Mismatches    8;  Indels    0;  Gaps    0;

Qy    602 ATTTATTTGAATCTACAAAAAACAACAAATAATTT 636
          ||  | ||||||  || ||||||  || |||||||
Db     14 ATGGACTTGAATTTAAAAAAAATAAAAAATAATCT 48


RESULT 15
AU268417
LOCUS       AU268417                 50 bp    mRNA    linear   EST 10-MAY-2002
DEFINITION  AU268417 VS Dictyostelium discoideum cDNA clone VSI266 5', mRNA
            sequence.
ACCESSION   AU268417
VERSION     AU268417.1  GI:20527215
KEYWORDS    EST.
SOURCE      Dictyostelium discoideum.
  ORGANISM  Dictyostelium discoideum
            Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
REFERENCE   1  (bases 1 to 50)
  AUTHORS   Urushihara,H., Morio,T., Saito,T., Koriki,E., Ochiai,H., Maeda,M.,
            Takeuchi,I., Kohara,Y. and Tanaka,Y.
  TITLE     Population analysis of cDNAs from unicellular and multicellular
            stages of Dictyostelium discoideum
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Hideko Urushihara
            Institute of Biological Sciences
            University of Tsukuba
            1-1-1 Tennoudai, Tsukuba, Ibaraki 305-8572, Japan
            Tel: 81-298-53-4664
            Fax: 81-298-53-6614
            Email: hideko@biol.tsukuba.ac.jp.
FEATURES             Location/Qualifiers
     source          1. .50
                     /organism="Dictyostelium discoideum"
                     /strain="AX4"
                     /db_xref="taxon:44689"
                     /clone="VSI266"
                     /clone_lib="VS"
                     /sex="mat A"
                     /dev_stage="vegetative"
BASE COUNT       30 a      1 c      3 g     16 t
ORIGIN

  Query Match             1.3%;  Score 22;  DB 9;  Length 50;
  Best Local Similarity   67.4%;  Pred. No. 4.2e+06;
  Matches   31;  Conservative    0;  Mismatches   15;  Indels    0;  Gaps    0;

Qy    578 GAACATACTTATATGTAAAGTATTATTTATTTGAATCTACAAAAAA 623
          ||| | ||  |||  |||| ||  |||| |||  ||  | ||||||
Db      5 GAAAAAACAAATAAATAAATTAAAATTTTTTTTTATAAAAAAAAAA 50


RESULT 16
BG179823
LOCUS       BG179823                 49 bp    mRNA    linear   EST 06-FEB-2001
DEFINITION  602329028F1 NIH_MGC_91 Homo sapiens cDNA clone IMAGE:4430262 5',
            mRNA sequence.
ACCESSION   BG179823
VERSION     BG179823.1  GI:12686526
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 49)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM10183  row: h  column: 07
            High quality sequence stop: 49.
FEATURES             Location/Qualifiers
     source          1. .49
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4430262"
                     /clone_lib="NIH_MGC_91"
                     /tissue_type="adenocarcinoma, cell line"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: prostate; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
                     Average insert size 1.4 kb. Library enriched for
                     full-length clones and constructed by Life Technologies.
                     Note: this is a NIH_MGC Library."
BASE COUNT       32 a      4 c      4 g      9 t
ORIGIN

  Query Match             1.3%;  Score 21.6;  DB 12;  Length 49;
  Best Local Similarity   68.2%;  Pred. No. 5e+06;
  Matches   30;  Conservative    0;  Mismatches   14;  Indels    0;  Gaps    0;

Qy   1177 TAGATAAATTTCAATCAGGGTTTTTAGATTAAACAAACAAACAA 1220
          || ||||||   ||  ||| |||  | | |||| ||| ||| ||
Db      5 TATATAAATAAAAACAAGGCTTTGGAAAATAAAAAAAAAAAAAA 48


RESULT 17
BI745472/c
LOCUS       BI745472                 49 bp    mRNA    linear   EST 25-SEP-2001
DEFINITION  rk81a10.y3 Meloidogyne javanica egg pAMP1 v6 Chiapelli McCarter
            Meloidogyne javanica cDNA 5', mRNA sequence.
ACCESSION   BI745472
VERSION     BI745472.1  GI:15767274
KEYWORDS    EST.
SOURCE      root-knot nematode.
  ORGANISM  Meloidogyne javanica
            Eukaryota; Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchina;
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            Tylenchoidea; Heteroderidae; Meloidogyninae; Meloidogyne.
REFERENCE   1  (bases 1 to 49)
  AUTHORS   McCarter,J., Clifton,S., Chiapelli,B., Pape,D., Martin,J., Wylie,T.
            , Dante,M., Marra,M., Hillier,L., Kucaba,T., Theising,B., Bowers,Y.
            , Gibbons,M., Ritter,E., Bennett,J., Franklin,C., Tsagareishvili,R.
            , Ronko,I., Kennedy,S., Maguire,L., Beck,C., Underwood,K., Steptoe
            ,M., Allen,M., Person,B., Swaller,T., Harvey,N., Schurk,R., Kohn,S.
            , Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and
            Wilson,R.
  TITLE     The Washington Univ. Nematode EST Project, 1999
  JOURNAL   Unpublished (1999)
COMMENT     Contact: McCarter JP
            The Washington Univ. Nematode EST Project, 1999
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            The library was constructed by Brandi Chiapelli and Dr. James
            McCarter (bchiapel@watson.wustl.edu & jmccarte@watson.wustl.edu) at
            Washington University, St. Louis. DNA Sequencing by: Washington
            University Genome Sequencing Center St. Louis.
            Putative full length read
            The vector to vector length is 50.
FEATURES             Location/Qualifiers
     source          1. .49
                     /organism="Meloidogyne javanica"
                     /db_xref="taxon:6303"
                     /clone_lib="Meloidogyne javanica egg pAMP1 v6 Chiapelli
                     McCarter"
                     /dev_stage="enriched for eggs"
                     /lab_host="DH10B"
                     /note="Vector: pAMP1 (Gibco); The library was constructed
                     by Brandi Chiapelli and Dr. James  McCarter at Washington
                     University, St. Louis. The cDNA was made by using Dynabead
                     oligo-dT priming (Dynal). PCR based library using a
                     modified  protocol from the SMART PCR cDNA Synthesis Kit
                     from Clontech. Directionally  cloned into the UDG sites of
                     pAMP1. Nematodes were provided by Dr. David  Bird of North
                     Carolina State University."
BASE COUNT       28 a      7 c      0 g     14 t
ORIGIN

  Query Match             1.3%;  Score 21.6;  DB 13;  Length 49;
  Best Local Similarity   68.2%;  Pred. No. 5e+06;
  Matches   30;  Conservative    0;  Mismatches   14;  Indels    0;  Gaps    0;

Qy   1158 ATATTAAATGATGTTTTATTAGATAAATTTCAATCAGGGTTTTT 1201
           || ||||||||  ||||| |   | | |||   | ||| |||||
Db     45 ATTTTAAATGAAATTTTAATTATTTATTTTGTGTAAGGTTTTTT 2


RESULT 18
AV957350/c
LOCUS       AV957350                 50 bp    mRNA    linear   EST 14-MAR-2002
DEFINITION  AV957350 Nori Satoh unpublished cDNA library, egg Ciona
            intestinalis cDNA clone cieg14i18 5', mRNA sequence.
ACCESSION   AV957350
VERSION     AV957350.1  GI:19445649
KEYWORDS    EST.
SOURCE      Ciona intestinalis.
  ORGANISM  Ciona intestinalis
            Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
            Phlebobranchia; Cionidae; Ciona.
REFERENCE   1  (bases 1 to 50)
  AUTHORS   Satoh,N., Satou,Y., Kohara,Y. and Shin-i,T.
  TITLE     Expressed genes in Ciona intestinalis
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Nori Satoh
            Department of Zoology
            Kyoto University
            Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
            Tel: 81-75-753-4081
            Fax: 81-75-705-1113
            Email: satoh@ascidian.zool.kyoto-u.ac.jp.
FEATURES             Location/Qualifiers
     source          1. .50
                     /organism="Ciona intestinalis"
                     /db_xref="taxon:7719"
                     /clone="cieg14i18"
                     /clone_lib="Nori Satoh unpublished cDNA library, egg"
                     /tissue_type="whole animal"
                     /dev_stage="egg"
                     /note="Vector: pBluescript SK"
BASE COUNT       13 a      0 c      2 g     31 t      4 others
ORIGIN

  Query Match             1.3%;  Score 21.6;  DB 10;  Length 50;
  Best Local Similarity   63.8%;  Pred. No. 5e+06;
  Matches   30;  Conservative    0;  Mismatches   17;  Indels    0;  Gaps    0;

Qy    600 TTATTTATTTGAATCTACAAAAAACAACAAATAATTTTTGAATATAA 646
          || ||| ||   |   | |||||| || ||| |  |||| || | ||
Db     49 TTTTTTTTTCCNAAAAAAAAAAAAAAAAAAAAAAANNTTTTAAAAAAAA 3


RESULT 19
BH853222
LOCUS       BH853222                 44 bp    DNA     linear   GSS 13-JUN-2002
DEFINITION  SALK_076208.37.05.x Arabidopsis thaliana TDNA insertion lines
            Arabidopsis thaliana genomic clone SALK_076208.37.05.x, DNA
            sequence.
ACCESSION   BH853222
VERSION     BH853222.1  GI:21424093
KEYWORDS    GSS.
SOURCE      thale cress.
  ORGANISM  Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1  (bases 1 to 44)
  AUTHORS   Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab
            ,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P.
            , Zimmerman,J. and Ecker,J.R.
  TITLE     A Sequence-Indexed Library of Insertion Mutations in the
            Arabidopsis Genome
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Joseph R. Ecker
            Salk Institute Genomic Analysis Laboratory (SIGnAL)
            The Salk Institute for Biological Studies
            10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
            Tel: 858 453 4100 x1752
            Fax: 858 558 6379
            Email: ecker@salk.edu
            This is single pass sequence recovered from the left border of
            TDNA.
            Class: TDNA tagged.
FEATURES             Location/Qualifiers
     source          1. .44
                     /organism="Arabidopsis thaliana"
                     /strain="Columbia 0"
                     /db_xref="taxon:3702"
                     /clone="SALK_076208.37.05.x"
                     /clone_lib="Arabidopsis thaliana TDNA insertion lines"
                     /note="PCR was performed on Arabidopsis thaliana lines
                     each of which contains  one or more TDNA insertion
                     elements. The resultant fragment for each  line was
                     directly sequenced to determine the genomic sequence at
                     the  site of insertion. Details of the protocols used can
                     be found at  http://signal.salk.edu/tdna_protocols.html"
BASE COUNT       15 a      4 c      6 g     19 t
ORIGIN

  Query Match             1.3%;  Score 21.4;  DB 17;  Length 44;
  Best Local Similarity   71.8%;  Pred. No. 5.6e+06;
  Matches   28;  Conservative    0;  Mismatches   11;  Indels    0;  Gaps    0;
```

```
Qy   1122 TTATAAAGATGTTATAGTAAATTTATTTTATTTTAGATA 1160
          ||  |||||||   |||  | |||||||| ||| ||| |
Db      3 TTTAAAAGATGACTTAGACATTTTATTTTCTTTAAGAAA 41


RESULT 20
BH850240
LOCUS       BH850240                 45 bp    DNA     linear   GSS 13-JUN-2002
DEFINITION  SALK_071000.50.25.x Arabidopsis thaliana TDNA insertion lines
            Arabidopsis thaliana genomic clone SALK_071000.50.25.x, DNA
            sequence.
ACCESSION   BH850240
VERSION     BH850240.1  GI:21421111
KEYWORDS    GSS.
SOURCE      thale cress.
  ORGANISM  Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1  (bases 1 to 45)
  AUTHORS   Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab
            ,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P.
            , Zimmerman,J. and Ecker,J.R.
  TITLE     A Sequence-Indexed Library of Insertion Mutations in the
            Arabidopsis Genome
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Joseph R. Ecker
            Salk Institute Genomic Analysis Laboratory (SIGnAL)
            The Salk Institute for Biological Studies
            10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
            Tel: 858 453 4100 x1752
            Fax: 858 558 6379
            Email: ecker@salk.edu
            This is single pass sequence recovered from the left border of
            TDNA.
            Class: TDNA tagged.
FEATURES             Location/Qualifiers
     source          1. .45
                     /organism="Arabidopsis thaliana"
                     /strain="Columbia 0"
                     /db_xref="taxon:3702"
                     /clone="SALK_071000.50.25.x"
                     /clone_lib="Arabidopsis thaliana TDNA insertion lines"
                     /note="PCR was performed on Arabidopsis thaliana lines
                     each of which contains  one or more TDNA insertion
                     elements. The resultant fragment for each  line was
                     directly sequenced to determine the genomic sequence at
                     the  site of insertion. Details of the protocols used can
                     be found at  http://signal.salk.edu/tdna_protocols.html"
BASE COUNT       16 a      2 c      5 g     22 t
ORIGIN

  Query Match             1.3%;  Score 21.4;  DB 17;  Length 45;
  Best Local Similarity   71.8%;  Pred. No. 5.6e+06;
  Matches   28;  Conservative    0;  Mismatches   11;  Indels    0;  Gaps    0;

Qy   1262 TAATTTTTTAGTATAAGTACATTATTGTTTATCTGAAAT 1300
          ||||||||||  |  |||  ||||   || |||||||
Db      7 TAATTTTTTAAAAATAGTTGATTAAATTTGATCTGAATT 45


Search completed: February  9, 2003, 19:20:11
Job time : 2368 secs
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GenCore version 5.1.3

OM nucleic - nucleic search, using sw model

Run on: February 9, 2003, 15:17:21 ; Search time 340 Seconds
(without alignments)
10855.957 Million cell updates/sec

Title: US-09-960-143-3
Perfect score: 1639
Sequence: 1 acaaactttcagagacagca.....atataatttgttgtcaaagt 1639

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 2166140

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_101002:*
1: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1980.DAT:*
2: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:*
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7: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1986.DAT:*
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9: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1988.DAT:*
10: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1989.DAT:*
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13: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1992.DAT:*
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20: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1999.DAT:*
21: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2000.DAT:*
22: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001A.DAT:*
23: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT:*
24: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
	1	37	2.3	37	18	AAT76272	Human MDNCF antise
c	2	37	2.3	37	20	AAX54069	Monocyte-derived n
c	3	37	2.3	37	21	AAF19635	Human monocyte der
c	4	37	2.3	37	21	AAA33513	Low adenosine anti
c	5	34	2.1	34	18	AAT76366	Human interleukin
c	6	34	2.1	34	20	AAX54167	Human IL-8 antisen
c	7	34	2.1	34	21	AAF19733	Human interleukin-
c	8	34	2.1	34	21	AAA33611	Low adenosine anti
c	9	33	2.0	33	14	AAQ37164	Anti-sense primer
c	10	33	2.0	33	17	AAT38979	Interleukin IL-8 3
c	11	33	2.0	33	20	AAV65360	Interleukin-8 anti
c	12	33	2.0	33	20	AAV08015	Primer IL-8 for In
c	13	31	1.9	31	18	AAT45913	Human interleukin-
	14	31	1.9	31	22	AAI30870	Human single nucle
	15	30	1.8	30	17	AAT45757	Human interleukin-
c	16	30	1.8	30	19	AAV61828	PCR primer for hum
c	17	30	1.8	30	19	AAV35562	Human interleukin
c	18	30	1.8	30	19	AAV35781	PCR primer IL8P2 o
c	19	30	1.8	30	22	AAC88174	Human interleukin
c	20	30	1.8	30	24	ABL46338	Human interleukin-
c	21	29	1.8	30	19	AAV24558	IL-8 antisense oli
	22	28	1.7	28	24	ABK66391	Human gene specifi
c	23	28	1.7	28	24	ABK66392	Human gene specifi
	24	26	1.6	26	24	AAD21908	PCR primer, 2767T
	25	25.2	1.5	39	18	AAT61103	Chimeric chemokine
c	26	25.2	1.5	39	18	AAT61104	Chimeric chemokine
c	27	25	1.5	25	17	AAT29243	Human interleukin-
c	28	25	1.5	25	18	AAT45912	Human interleukin-
	29	25	1.5	25	21	AAA65326	B-thromboglobulin
c	30	25	1.5	25	24	AAD39024	Human beta-actin s
c	31	25	1.5	25	24	AAD37345	Interleukin-8 (IL-
c	32	25	1.5	25	24	ABK14346	Human interleukin-
	33	25	1.5	26	24	AAD21907	PCR primer, 2767A
	34	24.4	1.5	48	18	AAT61099	Chimeric chemokine
	35	24	1.5	24	18	AAT45911	Human interleukin-
	36	24	1.5	24	24	AAD39023	Human beta-actin s
	37	24	1.5	24	24	AAD37344	Interleukin-8 (IL-
c	38	24	1.5	48	22	AAH30030	Human interleukin
	39	23.6	1.4	39	18	AAT61109	Chimeric chemokine
c	40	23.6	1.4	39	18	AAT61110	Chimeric chemokine
	41	23	1.4	23	17	AAT29242	Human interleukin-
c	42	23	1.4	23	18	AAT76365	Human interleukin
c	43	23	1.4	23	20	AAX54166	Human IL-8 antisen
c	44	23	1.4	23	21	AAF19732	Human interleukin-
c	45	23	1.4	23	21	AAA33610	Low adenosine anti

ALIGNMENTS

RESULT 1
AAT76272/c
ID AAT76272 standard; DNA; 37 BP.
XX
AC AAT76272;
XX
DT 15-SEP-1997 (first entry)
XX
DE Human MDNCF antisense oligonucleotide HSMDNCFAS2.
XX
KW Asthma; airway epithelium; adenosine free; cystic fibrosis;
KW chronic obstructive pulmonary disease; bronchitis;
KW monocyte-derived neutrophil chemotactic factor; ss.
XX
OS Synthetic.
XX
PN WO9640162-A1.
XX
PD 19-DEC-1996.
XX
PF 06-JUN-1996; 96WO-US09306.
XX
PR 07-JUN-1995; 95US-0474497.
XX
PA (UYEC-) UNIV EAST CAROLINA.
XX
PI Metzger WJ, Nyce JW;
XX
DR WPI; 1997-051871/05.
XX
PT Treatment of airway diseases such as asthma - by topically applying
PT adenosine-free antisense oligo:nucleotide to airway epithelium of

```
PT   subject
XX
PS   Claim 5; Page 33; 71pp; English.
XX
CC   A method for treating airway disease in a subject has been produced,
CC   which involves the topical administration of an essentially adenosine
CC   free antisense oligonucleotide (ON) to the airway epithelium of the
CC   subject. The present sequence is an antisense oligonucleotide
CC   HSMDNCFAS2 specific for the human monocyte-derived neutrophil
CC   chemotactic factor. The method can be used to treat airway diseases
CC   such as cystic fibrosis, asthma, chronic obstructive pulmonary disease,
CC   bronchitis and other airway diseases characterised by an inflammatory
CC   response. By eliminating adenosine from the antisense ON, its
CC   liberation upon antisense degradation is prevented, thereby preventing
CC   adenosine-induced bronchoconstriction in patients with hyper-reactive
CC   airways.
XX
SQ   Sequence 37 BP; 0 A; 11 C; 9 G; 17 T; 0 other;

  Query Match             2.3%;  Score 37;  DB 18;  Length 37;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+03;
  Matches   37;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      37 AGGACAAGAGCCAGGAAGAAACCACCGGAAGGAACCA 73
           |||||||||||||||||||||||||||||||||||||
Db      37 AGGACAAGAGCCAGGAAGAAACCACCGGAAGGAACCA 1


RESULT 2
AAX54069/c
ID   AAX54069 standard; DNA; 37 BP.
XX
AC   AAX54069;
XX
DT   05-JUL-1999  (first entry)
XX
DE   Monocyte-derived neutrophil chemotactic factor antisense oligo.
XX
KW   Antisense oligonucleotide; multiple target; antisense treatment;
KW   impaired respiration; inflammation; lung disease;
KW   pulmonary vasoconstriction; inflammation; allergic rhinitis;
KW   acute asthma; allergy; asthma; impeded respiration;
KW   respiratory distress syndrome; pain; cystic fibrosis;
KW   pulmonary hypertension; pulmonary vasoconstriction; emphysema;
KW   chronic obstructive pulmonary disease; leukemia; lymphoma; carcinoma;
KW   colon cancer; breast cancer; lung cancer; pancreatic cancer;
KW   hepatocellular carcinoma; kidney cancer; melanoma; hepatic metastasis;
KW   prostate cancer; ss.
XX
OS   Synthetic.
XX
PN   WO9913886-A1.
XX
PD   25-MAR-1999.
XX
PF   17-SEP-1998;   98WO-US19419.
XX
PR   09-JUN-1998;   98US-0093972.
PR   17-SEP-1997;   97US-0059160.
XX
PA   (UYEC-) UNIV EAST CAROLINA.
XX
PI   Nyce JW;
XX
DR   WPI; 1999-229400/19.
XX
PT   New antisense oligonucleotides used in treatment of, e.g. pulmonary
PT   vasoconstriction
XX
PS   Disclosure; Page 51; 120pp; English.
XX
CC   The specification describes antisense oligonucleotides (AAX52869-X55271)
CC   directed against at least 2 mRNAs selected from target genes, coding and
CC   non-coding regions of RNAs corresponding to target genes, gene
CC   initiation codons, genomic flanking regions, intron-exon borders, the
CC   5'-end, the 3'-end and the juxta-section between coding and non-coding
CC   regions and all segments of RNAs encoding proteins associated with one
CC   or more diseases, conditions or mixtures. The antisense oligonucleotides
CC   may be derived from sequences AAX55272-74. These multiple target
CC   oligonucleotides (specifically AAX55180-271) can be used for the
CC   antisense treatment of diseases and conditions. Typical diseases and
CC   conditions are those associated with impaired respiration and
CC   inflammation, including lung diseases, pulmonary vasoconstriction,
CC   inflammation, allergic rhinitis, acute asthma, allergies, asthma, impeded
CC   respiration, respiratory distress syndrome, pain, cystic fibrosis,
CC   pulmonary hypertension, pulmonary vasoconstriction, emphysema, chronic
CC   obstructive pulmonary disease (COPD), and cancers such as leukemias,
CC   lymphomas, carcinomas e.g. colon cancer, breast cancer, lung cancer,
CC   pancreatic cancer, hepatocellular carcinoma, kidney cancer, melanoma,
CC   hepatic metastases, as well as all types of cancers which may metastasize
CC   or have metastasized to the lungs, including breast and prostate cancer.
XX
SQ   Sequence 37 BP; 0 A; 11 C; 9 G; 17 T; 0 other;

  Query Match             2.3%;  Score 37;  DB 20;  Length 37;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+03;
  Matches   37;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      37 AGGACAAGAGCCAGGAAGAAACCACCGGAAGGAACCA 73
           |||||||||||||||||||||||||||||||||||||
Db      37 AGGACAAGAGCCAGGAAGAAACCACCGGAAGGAACCA 1


RESULT 3
AAF19635/c
ID   AAF19635 standard; DNA; 37 BP.
XX
AC   AAF19635;
XX
DT   14-MAR-2001  (first entry)
XX
DE   Human monocyte derived neutrophil chemotactic factor DNA fragment #1202.
XX
KW   Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
KW   human; airway disorder; bronchoconstriction; lung inflammation;
KW   surfactant depletion; respiratory; bronchodilator; antiinflammatory;
KW   immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic;
KW   respiratory obstruction; pulmonary obstruction; impeded respiration;
KW   surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
KW   respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
KW   pulmonary hypertension; emphysema; pulmonary transplantation rejection;
KW   chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
KW   cancer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200062736-A2.
XX
PD   26-OCT-2000.
XX
PF   24-MAR-2000; 2000WO-US08020.
XX
PR   06-APR-1999;   99US-0127958.
XX
PA   (UYEC-) UNIV EAST CAROLINA.
PA   (NYCE/) NYCE J W.
XX
PI   Nyce JW;
XX
DR   WPI; 2000-679539/66.
XX
PT   Low adenosine (A) content antisense oligonucleotides which do not
PT   trigger adenosine receptors during metabolism, useful e.g. for treating
PT   cancers and respiratory obstructions -
XX
PS   Claim 14; Page 210; 1592pp; English.
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XX
CC   The present invention describes low adenosine (A) content antisense
CC   oligonucleotides and compositions (I) comprising them. In the antisense
CC   oligonucleotides the A is replaced by a 'Universal' or alternative base.
CC   (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
CC   immunosuppressive, antiasthmatic, hypotensive and cytostatic activities.
CC   The antisense oligonucleotides and (I) can be used to down-regulate the
CC   expression and or activity of target polypeptides associated with
CC   lung/respiratory disorders and malignancies, such as stimulating and
CC   activating peptide factors and transmitters, transcription factors,
CC   immunoglobulins and antibodies, antibody receptors, cytokines and
CC   chemokines, endogenously produced specific and non-specific enzymes,
CC   binding proteins, adhesion molecules and their receptors, cytokine and
CC   chemokine receptors, adenosine receptors, bradykinin receptors, central
CC   nervous system (CNS) and peripheral nervous and non-nervous system
CC   receptors, CNS and peripheral nervous and non-nervous system peptide
CC   transmitters, defensins, growth factors, vasoactive peptides and
CC   receptors, binding proteins and malignancy associated proteins. The
CC   antisense oligonucleotides may be used in this way to treat disorders
CC   including respiratory obstruction (especially pulmonary obstruction
CC   and/or bronchoconstriction) and/or lung inflammation, allergy(ies)
CC   and/or surfactant hypoproduction which are associated with a disease or
CC   condition selected from pulmonary vasoconstriction, inflammation,
CC   allergies, asthma, impeded respiration, respiratory distress syndrome
CC   (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
CC   hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
CC   pulmonary transplantation rejection, pulmonary infections, bronchitis,
CC   and/or cancer. AAF18434 to AAF21543 represent human polynucleotide
CC   fragments and antisense oligonucleotides used in the exemplification of
CC   the present invention.
XX
SQ   Sequence 37 BP; 0 A; 11 C; 9 G; 17 T; 0 other;

  Query Match             2.3%;  Score 37;  DB 21;  Length 37;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+03;
  Matches   37;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      37 AGGACAAGAGCCAGGAAGAAACCACCGGAAGGAACCA 73
           |||||||||||||||||||||||||||||||||||||
Db      37 AGGACAAGAGCCAGGAAGAAACCACCGGAAGGAACCA 1


RESULT 4
AAA33513/c
ID   AAA33513 standard; DNA; 37 BP.
XX
AC   AAA33513;
XX
DT   28-JUL-2000  (first entry)
XX
DE   Low adenosine antisense oligonucleotide SEQ ID NO:1202.
XX
KW   Human; adenosine receptor; low adenosine antisense oligonucleotide;
KW   phosphorothioate; impaired respiration; inflammation; allergy;
KW   allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
KW   antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway;
KW   lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
KW   respiratory distress syndrome; pain; cystic fibrosis; emphysema;
KW   pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
KW   cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.
XX
OS   Homo sapiens.
XX
PN   WO200009525-A2.
XX
PD   24-FEB-2000.
XX
PF   03-AUG-1999;   99WO-US17712.
XX
PR   03-AUG-1998;   98US-0095212.
XX
PA   (UYEC-) UNIV EAST CAROLINA.
XX
PI   Nyce JW;
XX
DR   WPI; 2000-205971/18.
XX
PT   New antisense oligonucleotides useful for treating e.g. pulmonary
PT   vasoconstriction, inflammation, allergies, asthma, hypertension,
PT   bronchitis, emphysema, respiratory distress syndrome, ischemia or
PT   cancers -
XX
PS   Claim 18; Page 415; 1343pp; English.
XX
CC   The present invention describes a new composition comprising an
CC   antisense oligonucleotide (ON) with low adenosine (up to 15%), which
CC   targets nucleic acids involved in bronchoconstriction, allergies, and/or
CC   inflammation. The ON can have antiinflammatory, antiallergic,
CC   antiasthmatic, cytostatic and analgesic activities. The compositions are
CC   useful for the treatment of diseases associated with inflammation,
CC   impaired airways, including lung disease and diseases whose secondary
CC   effects afflict the lungs of a subject. They can be used for treating
CC   e.g. ischaemic conditions, pulmonary vasoconstriction, allergies,
CC   asthma, impeded respiration, respiratory distress syndrome, pain, cystic
CC   fibrosis, pulmonary hypertension, emphysema, chronic obstructive
CC   pulmonary disease (COPD), and cancers such as leukaemias, lymphomas,
CC   carcinomas, and cancers which may metastasise to the lungs, including
CC   breast and prostate cancer. The reduction of the adenosine content of
CC   the ONs reduces side effects. The A-containing ONs break down with the
CC   release of deoxyadenosine which activates adenosine receptors causing
CC   bronchoconstriction and inflammation. AAA32313 to AAA35312 represent the
CC   nucleotide sequences given in the sequence listing from the present
CC   invention, which correspond to SEQ ID NO:1 to 2815, and then the last
CC   185 sequences are also called SEQ ID NO:1 to 185, but the sequences
CC   differ from the previously named sequences. SEQ ID NO:11 to 1680
CC   (AAA32323 to AAA33992) are specifically claimed ONs from the present
CC   invention. N.B. Sequences given in the disclosure of the present
CC   invention do not match up with their corresponding SEQ ID NO: sequences
CC   given in the sequence listing.
XX
SQ   Sequence 37 BP; 0 A; 11 C; 9 G; 17 T; 0 other;

  Query Match             2.3%;  Score 37;  DB 21;  Length 37;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+03;
  Matches   37;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      37 AGGACAAGAGCCAGGAAGAAACCACCGGAAGGAACCA 73
           |||||||||||||||||||||||||||||||||||||
Db      37 AGGACAAGAGCCAGGAAGAAACCACCGGAAGGAACCA 1


RESULT 5
AAT76366/c
ID   AAT76366 standard; DNA; 34 BP.
XX
AC   AAT76366;
XX
DT   15-SEP-1997  (first entry)
XX
DE   Human interleukin 8 antisense oligonucleotide HUMIL8AAS3.
XX
KW   Asthma; airway epithelium; adenosine free; cystic fibrosis;
KW   chronic obstructive pulmonary disease; bronchitis; ss.
XX
OS   Synthetic.
XX
PN   WO9640162-A1.
XX
PD   19-DEC-1996.
XX
PF   06-JUN-1996;   96WO-US09306.
XX
PR   07-JUN-1995;   95US-0474497.
XX
PA   (UYEC-) UNIV EAST CAROLINA.
XX
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PI   Metzger WJ,  Nyce JW;
XX
DR   WPI; 1997-051871/05.
XX
PT   Treatment of airway diseases such as asthma - by topically applying
PT   adenosine-free antisense oligo:nucleotide to airway epithelium of
PT   subject
XX
PS   Claim 5; Page 36; 71pp; English.
XX
CC   A method for treating airway disease in a subject has been produced,
CC   which involves the topical administration of an essentially adenosine
CC   free antisense oligonucleotide (ON) to the airway epithelium of the
CC   subject. The present sequence is an antisense oligonucleotide
CC   HUMIL8AAS3 specific for the human interleukin 8. The method can
CC   be used to treat airway diseases such as cystic fibrosis, asthma,
CC   chronic obstructive pulmonary disease, bronchitis and other
CC   airway diseases characterised by an inflammatory response. By
CC   eliminating adenosine from the antisense ON, its liberation upon
CC   antisense degradation is prevented, thereby preventing adenosine-
CC   induced bronchoconstriction in patients with hyper-reactive airways.
XX
SQ   Sequence 34 BP; 0 A; 11 C; 7 G; 16 T; 0 other;

  Query Match             2.1%;  Score 34;  DB 18;  Length 34;
  Best Local Similarity   100.0%;  Pred. No. 4.5e+03;
  Matches   34;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      37 AGGACAAGAGCCAGGAAGAAACCACCGGAAGGAA 70
           ||||||||||||||||||||||||||||||||||
Db      34 AGGACAAGAGCCAGGAAGAAACCACCGGAAGGAA 1


RESULT 6
AAX54167/c
ID   AAX54167 standard; DNA; 34 BP.
XX
AC   AAX54167;
XX
DT   05-JUL-1999  (first entry)
XX
DE   Human IL-8 antisense oligonucleotide fragment.
XX
KW   Antisense oligonucleotide; multiple target; antisense treatment;
KW   impaired respiration; inflammation; lung disease;
KW   pulmonary vasoconstriction; inflammation; allergic rhinitis;
KW   acute asthma; allergy; asthma; impeded respiration;
KW   respiratory distress syndrome; pain; cystic fibrosis;
KW   pulmonary hypertension; pulmonary vasoconstriction; emphysema;
KW   chronic obstructive pulmonary disease; leukemia; lymphoma; carcinoma;
KW   colon cancer; breast cancer; lung cancer; pancreatic cancer;
KW   hepatocellular carcinoma; kidney cancer; melanoma; hepatic metastasis;
KW   prostate cancer; ss.
XX
OS   Synthetic.
XX
PN   WO9913886-A1.
XX
PD   25-MAR-1999.
XX
PF   17-SEP-1998;   98WO-US19419.
XX
PR   09-JUN-1998;   98US-0093972.
PR   17-SEP-1997;   97US-0059160.
XX
PA   (UYEC-) UNIV EAST CAROLINA.
XX
PI   Nyce JW;
XX
DR   WPI; 1999-229400/19.
XX
PT   New antisense oligonucleotides used in treatment of, e.g. pulmonary
PT   vasoconstriction
XX
PS   Disclosure; Page 55; 120pp; English.
XX
CC   The specification describes antisense oligonucleotides (AAX52869-X55271)
CC   directed against at least 2 mRNAs selected from target genes, coding and
CC   non-coding regions of RNAs corresponding to target genes, gene
CC   initiation codons, genomic flanking regions, intron-exon borders, the
CC   5'-end, the 3'-end and the juxta-section between coding and non-coding
CC   regions and all segments of RNAs encoding proteins associated with one
CC   or more diseases, conditions or mixtures. The antisense oligonucleotides
CC   may be derived from sequences AAX55272-74. These multiple target
CC   oligonucleotides (specifically AAX55180-271) can be used for the
CC   antisense treatment of diseases and conditions. Typical diseases and
CC   conditions are those associated with impaired respiration and
CC   inflammation, including lung diseases, pulmonary vasoconstriction,
CC   inflammation, allergic rhinitis, acute asthma, allergies, asthma, impeded
CC   respiration, respiratory distress syndrome, pain, cystic fibrosis,
CC   pulmonary hypertension, pulmonary vasoconstriction, emphysema, chronic
CC   obstructive pulmonary disease (COPD), and cancers such as leukemias,
CC   lymphomas, carcinomas e.g. colon cancer, breast cancer, lung cancer,
CC   pancreatic cancer, hepatocellular carcinoma, kidney cancer, melanoma,
CC   hepatic metastases, as well as all types of cancers which may metastasize
CC   or have metastasized to the lungs, including breast and prostate cancer.
XX
SQ   Sequence 34 BP; 0 A; 11 C; 7 G; 16 T; 0 other;

  Query Match             2.1%;  Score 34;  DB 20;  Length 34;
  Best Local Similarity   100.0%;  Pred. No. 4.5e+03;
  Matches   34;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      37 AGGACAAGAGCCAGGAAGAAACCACCGGAAGGAA 70
           ||||||||||||||||||||||||||||||||||
Db      34 AGGACAAGAGCCAGGAAGAAACCACCGGAAGGAA 1


RESULT 7
AAF19733/c
ID   AAF19733 standard; DNA; 34 BP.
XX
AC   AAF19733;
XX
DT   14-MAR-2001  (first entry)
XX
DE   Human interleukin-8 polynucleotide fragment #1300.
XX
KW   Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
KW   human; airway disorder; bronchoconstriction; lung inflammation;
KW   surfactant depletion; respiratory; bronchodilator; antiinflammatory;
KW   immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic;
KW   respiratory obstruction; pulmonary obstruction; impeded respiration;
KW   surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
KW   respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
KW   pulmonary hypertension; emphysema; pulmonary transplantation rejection;
KW   chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
KW   cancer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200062736-A2.
XX
PD   26-OCT-2000.
XX
PF   24-MAR-2000; 2000WO-US08020.
XX
PR   06-APR-1999;   99US-0127958.
XX
PA   (UYEC-) UNIV EAST CAROLINA.
PA   (NYCE/) NYCE J W.
XX
PI   Nyce JW;
XX
DR   WPI; 2000-679539/66.
XX
```

PT Low adenosine (A) content antisense oligonucleotides which do not
PT trigger adenosine receptors during metabolism, useful e.g. for treating
PT cancers and respiratory obstructions -
XX
PS Claim 14; Page 236; 1592pp; English.
XX
CC The present invention describes low adenosine (A) content antisense
CC oligonucleotides and compositions (I) comprising them. In the antisense
CC oligonucleotides the A is replaced by a 'Universal' or alternative base.
CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
CC immunosuppressive, antiasthmatic, hypotensive and cytostatic activities.
CC The antisense oligonucleotides and (I) can be used to down-regulate the
CC expression and or activity of target polypeptides associated with
CC lung/respiratory disorders and malignancies, such as stimulating and
CC activating peptide factors and transmitters, transcription factors,
CC immunoglobulins and antibodies, antibody receptors, cytokines and
CC chemokines, endogenously produced specific and non-specific enzymes,
CC binding proteins, adhesion molecules and their receptors, cytokine and
CC chemokine receptors, adenosine receptors, bradykinin receptors, central
CC nervous system (CNS) and peripheral nervous and non-nervous system
CC receptors, CNS and peripheral nervous and non-nervous system peptide
CC transmitters, defensins, growth factors, vasoactive peptides and
CC receptors, binding proteins and malignancy associated proteins. The
CC antisense oligonucleotides may be used in this way to treat disorders
CC including respiratory obstruction (especially pulmonary obstruction
CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies)
CC and/or surfactant hypoproduction which are associated with a disease or
CC condition selected from pulmonary vasoconstriction, inflammation,
CC allergies, asthma, impeded respiration, respiratory distress syndrome
CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
CC pulmonary transplantation rejection, pulmonary infections, bronchitis,
CC and/or cancer. AAF18434 to AAF21543 represent human polynucleotide
CC fragments and antisense oligonucleotides used in the exemplification of
CC the present invention.
XX
SQ Sequence 34 BP; 0 A; 11 C; 7 G; 16 T; 0 other;

Query Match 2.1%; Score 34; DB 21; Length 34;
Best Local Similarity 100.0%; Pred. No. 4.5e+03;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 37 AGGACAAGAGCCAGGAAGAAACCACCGGAAGGAA 70
||||||||||||||||||||||||||||||||||
Db 34 AGGACAAGAGCCAGGAAGAAACCACCGGAAGGAA 1

RESULT 8
AAA33611/c
ID AAA33611 standard; DNA; 34 BP.
XX
AC AAA33611;
XX
DT 28-JUL-2000 (first entry)
XX
DE Low adenosine antisense oligonucleotide SEQ ID NO:1300.
XX
KW Human; adenosine receptor; low adenosine antisense oligonucleotide;
KW phosphorothioate; impaired respiration; inflammation; allergy;
KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
KW antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway;
KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;
KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
KW cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.
XX
OS Homo sapiens.
XX
PN WO200009525-A2.
XX
PD 24-FEB-2000.
XX
PF 03-AUG-1999; 99WO-US17712.
XX
PR 03-AUG-1998; 98US-0095212.
XX
PA (UYEC-) UNIV EAST CAROLINA.
XX
PI Nyce JW;
XX
DR WPI; 2000-205971/18.
XX
PT New antisense oligonucleotides useful for treating e.g. pulmonary
PT vasoconstriction, inflammation, allergies, asthma, hypertension,
PT bronchitis, emphysema, respiratory distress syndrome, ischemia or
PT cancers -
XX
PS Claim 18; Page 427; 1343pp; English.
XX
CC The present invention describes a new composition comprising an
CC antisense oligonucleotide (ON) with low adenosine (up to 15%), which
CC targets nucleic acids involved in bronchoconstriction, allergies, and/or
CC inflammation. The ON can have antiinflammatory, antiallergic,
CC antiasthmatic, cytostatic and analgesic activities. The compositions are
CC useful for the treatment of diseases associated with inflammation,
CC impaired airways, including lung disease and diseases whose secondary
CC effects afflict the lungs of a subject. They can be used for treating
CC e.g. ischaemic conditions, pulmonary vasoconstriction, allergies,
CC asthma, impeded respiration, respiratory distress syndrome, pain, cystic
CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive
CC pulmonary disease (COPD), and cancers such as leukaemias, lymphomas,
CC carcinomas, and cancers which may metastasise to the lungs, including
CC breast and prostate cancer. The reduction of the adenosine content of
CC the ONs reduces side effects. The A-containing ONs break down with the
CC release of deoxyadenosine which activates adenosine receptors causing
CC bronchoconstriction and inflammation. AAA32313 to AAA35312 represent the
CC nucleotide sequences given in the sequence listing from the present
CC invention, which correspond to SEQ ID NO:1 to 2815, and then the last
CC 185 sequences are also called SEQ ID NO:1 to 185, but the sequences
CC differ from the previously named sequences. SEQ ID NO:11 to 1680
CC (AAA32323 to AAA33992) are specifically claimed ONs from the present
CC invention. N.B. Sequences given in the disclosure of the present
CC invention do not match up with their corresponding SEQ ID NO: sequences
CC given in the sequence listing.
XX
SQ Sequence 34 BP; 0 A; 11 C; 7 G; 16 T; 0 other;

Query Match 2.1%; Score 34; DB 21; Length 34;
Best Local Similarity 100.0%; Pred. No. 4.5e+03;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 37 AGGACAAGAGCCAGGAAGAAACCACCGGAAGGAA 70
||||||||||||||||||||||||||||||||||
Db 34 AGGACAAGAGCCAGGAAGAAACCACCGGAAGGAA 1

RESULT 9 102/103
AAQ37164/c
ID AAQ37164 standard; DNA; 33 BP.
XX
AC AAQ37164;
XX
DT 23-JUN-1993 (first entry)
XX
DE Anti-sense primer to amplify IL-8.
XX
KW Interleukin-8; polymerase chain reaction; PCR;
KW cytokine synthesis inhibitor; inflammation;
KW monokine production; Southern analysis; ss.
XX
OS Synthetic.
XX
PN WO9302693-A.
XX
PD 18-FEB-1993.
XX

```
PF   06-AUG-1992;   92WO-US06378.
XX
PR   06-AUG-1991;   91US-0742129.
XX
PA   (SCHE ) SCHERING CORP.
XX
PI   De Waal Malefyt R,  Howard M,  Hsu DH,  Ishida H,  OGarra A;
PI   Spits H,  Zlotnik A;
XX
DR   WPI; 1993-076172/09.
XX
PT   Use of interleukin-10 to modulate inflammation or T-cell mediated
PT   immune function - for treating septic and toxic shock,
PT   auto-immune diseases, tumours and infections diseases
XX
PS   Example B6; Page 87; 208pp; English.
XX
CC   To determine at which level IL-10 inhibited the production of
CC   cytokines by monocytes, comparative PCR analyses were performed on
CC   RNA isolated from monocytes, activated by LPS in the presence or
CC   absence of IL-10, IL-4 or the neutralising anti-IL-10 MAb for 24
CC   hours. mRNA isolated from the samples was reverse transcribed into
CC   cDNA and amplified by cytokine-specific primers. Primer AAQ37164 is
CC   specific to IL-8 (see AAQ37163 for sense primer). It was
CC   found that IL-1 alpha, IL-6, TNF alpha, GM-CSF and G-CSF expression
CC   was strongly inhibited by IL-10 and IL-4 at the mRNA level. IL-1 beta
CC   and IL-8 expression was only slightly affected by IL-10.
XX
SQ   Sequence 33 BP; 9 A; 10 C; 2 G; 12 T; 0 other;

  Query Match             2.0%;  Score 33;  DB 14;  Length 33;
  Best Local Similarity   100.0%;  Pred. No. 6.5e+03;
  Matches   33;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     358 GAGAAGTTTTTGAAGAGGGCTGAGAATTCATAA 390
           |||||||||||||||||||||||||||||||||
Db      33 GAGAAGTTTTTGAAGAGGGCTGAGAATTCATAA 1


RESULT 10
AAT38979/c
ID   AAT38979 standard; DNA; 33 BP.
XX
AC   AAT38979;
XX
DT   29-MAY-1997  (first entry)
XX
DE   Interleukin IL-8 3' PCR primer.
XX
KW   Cytokine; expression profile; genital wart; interleukin 12; IL-12;
KW   tumour regression; adjuvant; polymerase chain reaction; PCR;
KW   condyloma acuminata; human papilloma virus; HPV-6; HPV-11; HPV16;
KW   HPV18; anogenital; cutaneous; laryngeal; oesophageal; cancer; ss.
XX
OS   Synthetic.
XX
PN   WO9629091-A1.
XX
PD   26-SEP-1996.
XX
PF   22-MAR-1996;   96WO-GB00686.
XX
PR   22-MAR-1995;   95GB-0005784.
XX
PA   (UYCA-) UNIV CAMBRIDGE TECH SERVICES LTD.
XX
PI   Scarpini CG,  Stanley MA;
XX
DR   WPI; 1996-442947/44.
XX
PT   Use of interleukin-12 to treat papilloma virus-associated lesions -
PT   esp. as a vaccine adjuvant with papilloma virus antigen for
PT   immuno:therapy of warts or tumours
XX
PS   Disclosure; Page 14; 32pp; English.
XX
CC   RNA was extracted from genital lesions, reverse transcribed to
CC   produce cDNA and then the cDNA was used as the template for PCR
CC   amplification of various cytokines using the primers in AAT38964-
CC   AAT39005. To confirm the identity of amplified cDNA, digoxigenin-
CC   labelled probes specific for each cytokine (see AAT39006-T39021)
CC   were hybridised with Southern blots of amplified sequences. The
CC   expression profile for regressing and non-regressing warts was
CC   established and compared to cytokine expression patterns in normal
CC   cervical tissue. Results showed that interleukin 12 is barely
CC   expressed (if at all) in non-regressing warts, but is expressed in
CC   regressing warts. This suggests a central role for IL-12 in wart
CC   regression. It has been found that IL-12 can be used (especially
CC   as a vaccine adjuvant) for treating papilloma virus-associated
CC   lesions such as condyloma acuminata (anogenital warts) caused by
CC   human papilloma virus type 6 (HPV-6) and/or HPV-11 and more
CC   generally for treatment of tumours associated with HPV16 and HPV18
CC   infection e.g. anogenital, cutaneous, laryngeal and oesophageal
CC   cancers.
XX
SQ   Sequence 33 BP; 9 A; 10 C; 2 G; 12 T; 0 other;

  Query Match             2.0%;  Score 33;  DB 17;  Length 33;
  Best Local Similarity   100.0%;  Pred. No. 6.5e+03;
  Matches   33;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     358 GAGAAGTTTTTGAAGAGGGCTGAGAATTCATAA 390
           |||||||||||||||||||||||||||||||||
Db      33 GAGAAGTTTTTGAAGAGGGCTGAGAATTCATAA 1


RESULT 11
AAV65360/c
ID   AAV65360 standard; DNA; 33 BP.
XX
AC   AAV65360;
XX
DT   22-JAN-1999  (first entry)
XX
DE   Interleukin-8 antisense primer.
XX
KW   Interleukin; IL-10; IL-6; IL-8; inflammatory response; endotoxin;
KW   tumour necrosis factor alpha; TNF; IL-1 alpha; IL-1 beta; bacteria;
KW   septic; toxic shock; superantigen; T-cell dependent response; human;
KW   viral; PCR primer; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   US5837293-A.
XX
PD   17-NOV-1998.
XX
PF   07-JUN-1995;   95US-0481560.
XX
PR   24-MAR-1995;   95US-0410654.
PR   06-AUG-1991;   91US-0742129.
PR   06-AUG-1992;   92US-0926853.
PR   19-APR-1994;   94US-0229854.
PR   07-JUN-1995;   95US-0481560.
XX
PA   (SCHE ) SCHERING CORP.
XX
PI   De Waal Malefyt R,  Howard M,  Hsu D,  Ishida H,  O'Garra A;
PI   Spits H,  Zlotnik A;
XX
DR   WPI; 1999-023391/02.
XX
PT   Reducing inflammatory response by treatment with interleukin-10 -
PT   particularly for treating bacterial infections, e.g. septic or toxic
PT   shock
```

```
XX
PS   Example 14; Column 42; 108pp; English.
XX
CC   Sequences AAV65353 to AAV65370 represent PCR primers used during the
CC   course of the invention. The invention provides a method for reducing
CC   inflammatory response characterised by elevated levels of interleukin
CC   (IL)-1 alpha, IL-1 beta, IL-6 or IL-8, or of tumour necrosis factor
CC   (TNF) alpha which comprises administering IL-10. The IL-10 to be
CC   administered is a recombinant mature protein selected from the sequences
CC   of human IL-10 (AAW81421, AAW81423) or viral IL-10 (AAW81422, AAW81423).
CC   IL-10 is especially administered to humans at risk of developing an
CC   inflammatory response, particularly where this is caused by infection by
CC   gram-positive or negative bacteria that produce endotoxins. Specific
CC   applications are in cases of septic or toxic shock and where infection
CC   results in a T-cell dependent response. Treatment with IL-10 reduces
CC   levels of the proinflammatory cytokines (by reducing their synthesis in
CC   monocytes, macrophages and natural killer cells), and inhibits activation
CC   of T cells by superantigens.
XX
SQ   Sequence 33 BP; 9 A; 10 C; 2 G; 12 T; 0 other;

  Query Match             2.0%;  Score 33;  DB 20;  Length 33;
  Best Local Similarity   100.0%;  Pred. No. 6.5e+03;
  Matches   33;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     358 GAGAAGTTTTTGAAGAGGGCTGAGAATTCATAA 390
           |||||||||||||||||||||||||||||||||
Db      33 GAGAAGTTTTTGAAGAGGGCTGAGAATTCATAA 1


RESULT 12
AAV08015/c
ID   AAV08015 standard; DNA; 33 BP.
XX
AC   AAV08015;
XX
DT   20-JAN-1999  (first entry)
XX
DE   Primer IL-8 for Interleukin-10 coding sequence.
XX
KW   Interleukin-10; IL-10; septic shock; bacterial infection; toxic shock;
KW   infectious shock; inflammation; immune response modulation; therapy;
KW   PCR primer; ss.
XX
OS   Synthetic.
XX
PN   US5833976-A.
XX
PD   10-NOV-1998.
XX
PF   24-MAR-1995;   95US-0410654.
XX
PR   06-AUG-1992;   92US-0926853.
PR   06-AUG-1991;   91US-0742129.
PR   19-APR-1994;   94US-0229854.
PR   24-MAR-1995;   95US-0410654.
XX
PA   (SCHE ) SCHERING CORP.
XX
PI   De Waal Malefyt R,  Howard M,  Hsu D,  Ishida H,  O'Garra A;
PI   Spits H,  Zlotnik A;
XX
DR   WPI; 1999-008644/01.
XX
PT   Treating shock conditions from e.g. bacterial infections - comprises
PT   administering interleukin-10
XX
PS   Example 14; Column 43; 109pp; English.
XX
CC   This sequence represents a primer for a interleukin-10 (IL-10) coding
CC   sequence. The IL-10 protein can be used in the method of the invention
CC   for ameliorating a symptom of: (a) septic shock in a host suffering from
CC   a bacterial (preferably gram negative) infection; (b) toxic shock;
CC   (c) infectious shock; or (d) inflammation. The method comprises
CC   administering a biologically active IL-10 (preferably human) protein,
CC   analogue or a fragment (preferably full length). The treatment is used to
CC   modulate immune responses caused by the different shock syndromes, which
CC   are endotoxin or superantigen induced toxicity, or autoimmune related
CC   conditions. The conditions are side-effects of microbial infections,
CC   caused by release of their protein products, especially on anti-microbial
CC   treatment, which when cells are killed, they lyse, releasing proteins
CC   which induce the shock conditions. IL-10 inhibits TNF-alpha (tumour
CC   necrosis factor-alpha) and TNF-gamma synthesis, which as part of an
CC   immune response elicits the shock syndromes.
XX
SQ   Sequence 33 BP; 9 A; 10 C; 2 G; 12 T; 0 other;

  Query Match             2.0%;  Score 33;  DB 20;  Length 33;
  Best Local Similarity   100.0%;  Pred. No. 6.5e+03;
  Matches   33;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     358 GAGAAGTTTTTGAAGAGGGCTGAGAATTCATAA 390
           |||||||||||||||||||||||||||||||||
Db      33 GAGAAGTTTTTGAAGAGGGCTGAGAATTCATAA 1


RESULT 13
AAT45913/c
ID   AAT45913 standard; DNA; 31 BP.
XX
AC   AAT45913;
XX
DT   01-SEP-1997  (first entry)
XX
DE   Human interleukin-8 PCR product hybridisation probe.
XX
KW   Interleukin 8; IL-8; polymerase chain reaction; PCR primer;
KW   detection; diagnosis; cytokine; renal transplant rejection;
KW   immunoassay; detergent chaotrope; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1
FT                   /*tag=  a
FT                   /note= "labelled with FITC"
XX
PN   WO9639536-A1.
XX
PD   12-DEC-1996.
XX
PF   31-MAY-1996;   96WO-US08142.
XX
PR   06-JUN-1995;   95US-0467909.
XX
PA   (TCEL-) T CELL DIAGNOSTICS INC.
XX
PI   Emmett C,  Foster KA;
XX
DR   WPI; 1997-043157/04.
XX
PT   Quantification of mRNA expression levels - using universal enzyme
PT   linked immunosorbent assay, for rapid diagnosis of disease and
PT   transplant rejection
XX
PS   Example 5; Page 10; 19pp; English.
XX
CC   A new method for the quantification of mRNA expression levels can
CC   be used for detecting the cytokine interleukin-8. In the method,
CC   total RNA is extracted from a sample, preferably using a detergent
CC   chaotrope lysis mixture, and cDNA is synthesised from mRNA. This
CC   cDNA is added to nucleotides, Taq polymerase, a magnesium source,
CC   a 3'-primer and a 5'-primer labelled with a molecule capable of
CC   binding to a coated microtitre plate and a PCR reaction is performed.
CC   A probe, capable of hybridising to the PCR product and labelled with
CC   a detectable marker or containing a molecule capable of binding to
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CC   an agent coated on a microtitre plate is added to the PCR product. A
CC   mixture of hybridised probe and PCR product, unhybridised probe and
CC   PCR products and excess primers are transferred to a microtitre plate
CC   coated with an agent capable of binding to a molecule on the PCR
CC   product, or the molecule on the probe. The detectable marker is
CC   detected on a bound hybridised probe and PCR product, preferably
CC   via the detection of an antibody that detects the labelled primer
CC   or probe, so that mRNA levels can be determined. Primer and probe
CC   sequences which can be used for the detection of interleukin-8
CC   include the present sequence.
XX
SQ   Sequence 31 BP; 11 A; 8 C; 9 G; 3 T; 0 other;

  Query Match             1.9%;  Score 31;  DB 18;  Length 31;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+04;
  Matches   31;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    119 TGGCAGCCTTCCTGATTTCTGCAGCTCTGTG 149
          |||||||||||||||||||||||||||||||
Db     31 TGGCAGCCTTCCTGATTTCTGCAGCTCTGTG 1


RESULT 14
AAI30870
ID   AAI30870 standard; DNA; 31 BP.
XX
AC   AAI30870;
XX
DT   18-OCT-2001  (first entry)
XX
DE   Human single nucleotide polymorphism (SNP) IL8.
XX
KW   Human; resequence; genotype; disease; forensic; paternity testing;
KW   single nucleotide polymorphism; SNP; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Variation       replace(16,C)
FT                   /*tag= a
FT                   /standard_name= "single nucleotide polymorphism"
XX
PN   WO200166800-A2.
XX
PD   13-SEP-2001.
XX
PF   07-MAR-2001; 2001WO-US07268.
XX
PR   07-MAR-2000; 2000US-0187510.
PR   22-MAY-2000; 2000US-0206129.
XX
PA   (WHED ) WHITEHEAD INST BIOMEDICAL RES.
XX
PI   Cargill M,  Ireland JS,  Lander ES;
XX
DR   WPI; 2001-522952/57.
XX
PT   Nucleic acid molecules from the human genome which include polymorphic
PT   sites, useful in methods for predicting the presence, absence or
PT   severity of a particular phenotype or disorder (e.g. diabetes)
PT   associated with a particular genotype -
XX
PS   Claim 1; Page 113; 145pp; English.
XX
CC   The invention relates to the identification of nucleic acid molecules
CC   (AAI29513-AAI31314) from the human genome which include polymorphic sites
CC   which can predispose individuals to disease. Various genes from a number
CC   of individuals were resequenced and single nucleotide polymorphisms
CC   (SNPs) in these genes discovered. The method is useful for predicting the
CC   presence, absence or severity of a particular phenotype or disorder (e.g.
CC   diabetes) associated with a particular genotype. The nucleic acids
CC   containing the polymorphic sites may be useful in forensics and paternity
CC   testing.
XX
SQ   Sequence 31 BP; 12 A; 8 C; 4 G; 7 T; 0 other;

  Query Match             1.9%;  Score 31;  DB 22;  Length 31;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+04;
  Matches   31;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    220 TTCCACCCCAAATTTATCAAAGAACTGAGAG 250
          |||||||||||||||||||||||||||||||
Db      1 TTCCACCCCAAATTTATCAAAGAACTGAGAG 31


RESULT 15
AAT45757
ID   AAT45757 standard; DNA; 30 BP.
XX
AC   AAT45757;
XX
DT   17-FEB-1997  (first entry)
XX
DE   Human interleukin-8 gene probe.
XX
KW   Polymerase chain reaction; PCR; interleukin; IL; cytokine;
KW   growth factor; animal model; stem cell; haematopoiesis; CD34;
KW   infection; HIV; human immunodeficiency virus; immunomodulator;
KW   immortalise; bone marrow; stromal cell; engraftment; determination;
KW   study; research; ss.
XX
OS   Homo sapiens.
XX
PN   WO9617627-A2.
XX
PD   13-JUN-1996.
XX
PF   08-DEC-1995;   95WO-US15986.
XX
PR   09-DEC-1994;   94US-0352957.
XX
PA   (GART/) GARTNER S.
PA   (HALL/) HALL E.
PA   (KAUS/) KAUSHAL S.
PA   (KESS/) KESSLER S.
PA   (LRUS/) LA RUSSA V.
PA   (MOSC/) MOSCA J D.
XX
PI   Gartner S,  Hall E,  Kaushal S,  Kessler S,  La Russa V;
PI   Mosca JD;
XX
DR   WPI; 1996-286928/29.
XX
PT   Animal models for human haematopoiesis - have en-grafted human or
PT   primate stem cells in the presence of immortalised bone marrow
PT   stromal cells
XX
PS   Example 1; Page 15; 43pp; English.
XX
CC   AAT45754-T45762 are probes used to determine whether or not the
CC   cytokines IL-1, IL-6, IL-8, GM-CSF, G-CSF, M-CSF, TGF-alpha and
CC   stem cell factor are expressed by a human bone marrow stromal
CC   cell line, Lof(11-10). The cells were found to produce the cytokines
CC   which support the growth of CD34+ stem cells. The Lof(11-10) cells
CC   were injected into SCID mice (previously irradiated to provide an
CC   internal space for CD34+ cells to populate). Five to seven days
CC   after injection the mice were injected with 3 to 5 human CD34+ cells.
CC   After 3 weeks, human CD34+ cells were found in the bone marrow of
CC   the mice. The immortalised bone marrow stem cells create a human
CC   microenvironment supplying human cytokines in the animals to provide
CC   for the engraftment, maintenance and differentiation of CD34+ stem
CC   cells. Animal models created by administering Lof(11-10) cells are
CC   used to study and determine the effectiveness of therapies against
CC   disease such as HIV infection. They can also be used to assay for
CC   haematopoietic growth factors, immunomodulators and/or immune
CC   toxins.
```

```
XX
SQ   Sequence 30 BP; 10 A; 5 C; 10 G; 5 T; 0 other;

  Query Match             1.8%;  Score 30;  DB 17;  Length 30;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+04;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     241 GAACTGAGAGTGATTGAGAGTGGACCACAC 270
           ||||||||||||||||||||||||||||||
Db       1 GAACTGAGAGTGATTGAGAGTGGACCACAC 30


RESULT 16
AAV61828/c
ID   AAV61828 standard; DNA; 30 BP.
XX
AC   AAV61828;
XX
DT   15-JAN-1999  (first entry)
XX
DE   PCR primer for human GISP coding sequence.
XX
KW   Glucocorticoid inducible suppressor protein; interleukin-8; rheumatism;
KW   intracellular signal transmission inhibitor; IL-8 promoter; allergy;
KW   inflammatory disease; bronchial asthma; therapy; PCR primer; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   WO9838213-A1.
XX
PD   03-SEP-1998.
XX
PF   27-FEB-1998;   98WO-JP00836.
XX
PR   28-FEB-1997;   97JP-0062008.
XX
PA   (CYTO-) INST CYTOSIGNAL RES INC.
XX
PI   Ohtsuka T,  Yoshida H;
XX
DR   WPI; 1998-481142/41.
XX
PT   Protein inhibiting activation of interleukin-8 promoter in response
PT   to extracellular stimulus - for use in diseases involving
PT   interleukin-8 expression, such as inflammatory disorders and asthma
XX
PS   Example 5; Page 56; 72pp; Japanese.
XX
CC   This sequence represents a PCR primer for DNA encoding the human
CC   glucocorticoid inducible suppressor protein (GISP) of the invention. The
CC   GISP is a intracellular signal transmission inhibitor, and inhibits the
CC   activation of interleukin-8 (IL-8) promoter activity in response to a
CC   specific extracellular stimulus (especially by interleukin-1 beta). The
CC   invention can be used in the treatment and prevention of disorders in
CC   which IL-8 expression is involved, such as inflammatory diseases,
CC   bronchial asthma, allergy and rheumatism.
XX
SQ   Sequence 30 BP; 3 A; 7 C; 8 G; 12 T; 0 other;

  Query Match             1.8%;  Score 30;  DB 19;  Length 30;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+04;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      14 GACAGCAGAGCACACAAGCTTCTAGGACAA 43
           ||||||||||||||||||||||||||||||
Db      30 GACAGCAGAGCACACAAGCTTCTAGGACAA 1


RESULT 17
AAV35562/c
ID   AAV35562 standard; DNA; 30 BP.
XX
AC   AAV35562;
XX
DT   24-SEP-1998  (first entry)
XX
DE   Human interleukin 18 promoter PCR primer #2 from WO9822581 Example 1.
XX
KW   Transcription repressor protein; inflammatory disease; regulator;
KW   interleukin 8; IL-8; rheumatoid arthritis; asthma; ringworm;
KW   skin inflammation; septic shock; gene therapy; MRC-5 SV1 TG1 cell;
KW   PCR primer; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   WO9822581-A1.
XX
PD   28-MAY-1998.
XX
PF   12-NOV-1997;   97WO-JP04127.
XX
PR   15-NOV-1996;   96JP-0305043.
XX
PA   (CYTO-) INST CYTOSIGNAL RES INC.
XX
PI   Nagasawa Y,  Yoshida H;
XX
DR   WPI; 1998-312467/27.
XX
PT   Transcription repressor protein for treatment of inflammatory
PT   diseases - consists of transcription regulating protein having part
PT   deleted which is not involved in DNA binding
XX
PS   Example 1; Page 12; 62pp; Japanese.
XX
CC   The present sequence represents a PCR primer used in an example from the
CC   present invention. The present invention describes a protein which has
CC   transcription repressor activity and consists of a transcription
CC   regulator protein from which a part (not involved in DNA binding) has
CC   been deleted, or derived from such a protein by addition, deletion or
CC   substitution of one or more amino acid residues. In particular, the
CC   protein is one which inhibits the transcription of the interleukin-8
CC   (IL-8) gene. The protein is used for the treatment and prevention of
CC   disorders such as inflammatory diseases mediated by interleukin-8, e.g.
CC   rheumatoid arthritis, asthma, ringworm, skin inflammation, septic shock.
CC   The DNA encoding the protein may be used in gene therapy.
XX
SQ   Sequence 30 BP; 3 A; 7 C; 8 G; 12 T; 0 other;

  Query Match             1.8%;  Score 30;  DB 19;  Length 30;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+04;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      14 GACAGCAGAGCACACAAGCTTCTAGGACAA 43
           ||||||||||||||||||||||||||||||
Db      30 GACAGCAGAGCACACAAGCTTCTAGGACAA 1


RESULT 18
AAV35781/c
ID   AAV35781 standard; DNA; 30 BP.
XX
AC   AAV35781;
XX
DT   22-SEP-1998  (first entry)
XX
DE   PCR primer IL8P2 of the invention.
XX
KW   Induce; apoptosis; guanine phosphoribosyltransferase; gpt; luciferase;
KW   cytokine; tumour necrosis factor; interleukin-1; inhibitory effect;
KW   intracellular signal transmission; PCR primer; ss.
XX
OS   Synthetic.
XX
```

PN WO9822578-A1.
XX
PD 28-MAY-1998.
XX
PF 12-NOV-1997; 97WO-JP04126.
XX
PR 15-NOV-1996; 96JP-0305163.
XX
PA (CYTO-) INST CYTOSIGNAL RES INC.
XX
PI Nagasawa Y, Yoshida H;
XX
DR WPI; 1998-312464/27.
XX
PT Test system for detecting intra-cellular signal transmission
PT inhibition - using vector containing apoptosis-inhibiting or
PT reporter gene and promoter sequence, used for, e.g. screening for
PT potential anti-inflammatory agents
XX
PS Example 1; Page 20; 62pp; Japanese.
XX
CC PCR primers AAV35780-81 are used in the course of the invention. The
CC specification describes plasmid vectors which comprise a gene which
CC can induce apoptosis under specific conditions, e.g. guanine
CC phosphoribosyltransferase (gpt)), or a reporter gene, e.g. luciferase,
CC where the gene is situated downstream of a promoter which responds to
CC specific extracellular stimulation such as the presence of a cytokine,
CC e.g. tumour necrosis factor (TNF) or interleukin-1. The vector may be
CC used to transform a suitable cell line, such as a cell line which does
CC not produce hypoxanthine-guanine phosphoribosyl transferase (HGPRT). The
CC transformed cells are used to test the inhibitory effect of a gene or
CC substance on intracellular signal transmission.
XX
SQ Sequence 30 BP; 3 A; 7 C; 8 G; 12 T; 0 other;

Query Match 1.8%; Score 30; DB 19; Length 30;
Best Local Similarity 100.0%; Pred. No. 2.1e+04;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 GACAGCAGAGCACACAAGCTTCTAGGACAA 43
||||||||||||||||||||||||||||||
Db 30 GACAGCAGAGCACACAAGCTTCTAGGACAA 1

RESULT 19
AAC88174/c
ID AAC88174 standard; DNA; 30 BP.
XX
AC AAC88174;
XX
DT 14-MAR-2001 (first entry)
XX
DE Human interleukin 8 5'-regulatory sequence PCR primer SEQ ID NO:3.
XX
KW Human; interleukin 8; IL-8; regulation; point mutation; NF-kappa B;
KW AP-1 binding site; interleukin 1 beta; tumour necrosis factor alpha;
KW promoter; antiinflammatory; antiarteriosclerotic; screening; inhibitor;
KW identification; inflammation; arteriosclerosis; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO200071697-A1.
XX
PD 30-NOV-2000.
XX
PF 24-MAY-2000; 2000WO-JP03326.
XX
PR 24-MAY-1999; 99JP-0143032.
XX
PA (SANY) SANKYO CO LTD.
XX
PI Koishi R, Yoshimura C, Serizawa N;
XX
DR WPI; 2001-112080/12.
XX
PT Screening for potential inhibitors of the NF-kappa-B activation
PT pathway, useful for treatment of inflammation and arteriosclerosis -
XX
PS Example 1; Page 15; 49pp; Japanese.
XX
CC The present invention describes a method for screening for potential
CC specific inhibitors of pathways activated by interleukin (IL)-1 beta,
CC tumour necrosis factor (TNF) alpha or a leustrodaxin derivative, by
CC culturing a cell transformed by a marker gene controlled by a promoter
CC gene containing a NF-kappa-B binding site in the presence of
CC IL1beta/TNFalpha/leustrodaxin derivative and the inhibitor and observing
CC the degree of marker gene expression. Also described is a method for
CC activating a promoter gene containing a NF-kappa-B binding site and
CC inhibitors identified by the above method. The method can be used for
CC the identification of inhibitors of the NF-kappa-B activation pathway
CC which can be used for the treatment of inflammation and arteriosclerosis.
CC The present sequence represents a PCR primer for the 5'-regulatory
CC sequence of the human IL-8 gene, which is used in an example from the
CC present invention.
XX
SQ Sequence 30 BP; 3 A; 7 C; 8 G; 12 T; 0 other;

Query Match 1.8%; Score 30; DB 22; Length 30;
Best Local Similarity 100.0%; Pred. No. 2.1e+04;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 GACAGCAGAGCACACAAGCTTCTAGGACAA 43
||||||||||||||||||||||||||||||
Db 30 GACAGCAGAGCACACAAGCTTCTAGGACAA 1

RESULT 20
ABL46338/c
ID ABL46338 standard; DNA; 30 BP.
XX
AC ABL46338;
XX
DT 26-APR-2002 (first entry)
XX
DE Human interleukin-1 beta oligonucleotide SEQ ID NO:305.
XX
KW Nucleic acid accessible hybridisation site; detection; hybridisation;
KW characterisation; identification; nucleic acid structure; diagnosis;
KW PCR primer; probe; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200198537-A2.
XX
PD 27-DEC-2001.
XX
PF 15-JUN-2001; 2001WO-US19401.
XX
PR 17-JUN-2000; 2000US-212308P.
PR 15-JUN-2001; 2001US-0212308.
XX
PA (THIR-) THIRD WAVE TECHNOLOGIES INC.
XX
PI Lyamichev V, Allawi H, Dong F, Neri BP, Vener IT;
XX
DR WPI; 2002-049698/06.
XX
PT Identifying oligonucleotides hybridizing to nucleic acids containing
PT secondary structure, useful in clinical diagnosis, comprises
PT identifying primers that interact with the target to form an extension
PT product under amplification conditions -
XX
PS Claim 48; Fig 81A; 409pp; English.
XX
CC The present invention describes a method for identifying oligonucleotides

CC with desired hybridisation properties to nucleic acid targets containing
CC secondary structure. The method comprises amplifying a target nucleic
CC acid having at least one accessible and one inaccessible site. Primers
CC that form an extension product are identified as the oligonucleotides
CC which can interact with the folded target nucleic acid. Oligonucleotides
CC from the present invention can be used in novel detection methods for
CC clinical diagnostic purposes, including the detection and identification
CC of pathogenic organisms (e.g. HIV). The method allows the ability to
CC rapidly analyse nucleic acid structures. ABL46034 to ABL46367 represent
CC sequences used in the exemplification of the present invention.
XX
SQ Sequence 30 BP; 13 A; 4 C; 2 G; 11 T; 0 other;

Query Match 1.8%; Score 30; DB 24; Length 30;
Best Local Similarity 100.0%; Pred. No. 2.1e+04;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1165 ATGATGTTTTATTAGATAAATTTCAATCAG 1194
||||||||||||||||||||||||||||||
Db 30 ATGATGTTTTATTAGATAAATTTCAATCAG 1

Search completed: February 9, 2003, 17:30:46
Job time : 350 secs

GenCore version 5.1.3

OM nucleic - nucleic search, using sw model

Run on: February 9, 2003, 15:52:56 ; Search time 4173 Seconds
(without alignments)
11430.505 Million cell updates/sec

Title: US-09-960-143-3
Perfect score: 1639
Sequence: 1 acaaactttcagagacagca.....atataatttgttgtcaaagt 1639

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 841850

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
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23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vi:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rod:*
36: em_htg_mam:*
37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	37.4	2.3	47	6	AR021184	AR021184 Sequence
2	37.4	2.3	47	6	I60565	I60565 Sequence 42
c 3	37	2.3	37	6	AR021182	AR021182 Sequence
c 4	37	2.3	37	6	I60563	I60563 Sequence 40
c 5	33	2.0	33	6	A56958	A56958 Sequence 16
c 6	33	2.0	33	6	AR052918	AR052918 Sequence
c 7	33	2.0	33	6	AR054281	AR054281 Sequence
c 8	33	2.0	33	6	AR054483	AR054483 Sequence
9	30.6	1.9	31	6	AX249279	AX249279 Sequence
c 10	30	1.8	30	6	AR200024	AR200024 Sequence
c 11	30	1.8	30	6	AX419968	AX419968 Sequence
c 12	30	1.8	30	6	BD004257	BD004257 Method fo
c 13	29	1.8	29	6	AX317616	AX317616 Sequence
14	28	1.7	28	6	AR090359	AR090359 Sequence
c 15	28	1.7	28	6	AR090360	AR090360 Sequence
16	28	1.7	28	6	AR197394	AR197394 Sequence
c 17	28	1.7	28	6	AR197395	AR197395 Sequence
18	26	1.6	26	6	AX280042	AX280042 Sequence
c 19	25	1.5	25	6	I22270	I22270 Sequence 8
20	25	1.5	26	6	AX280041	AX280041 Sequence
c 21	24	1.5	24	6	AR207732	AR207732 Sequence
22	23	1.4	23	6	I22269	I22269 Sequence 7
23	23	1.4	40	6	AR021188	AR021188 Sequence
c 24	22.8	1.4	31	6	AX203829	AX203829 Sequence
25	22.8	1.4	48	6	AX426642	AX426642 Sequence
26	22.6	1.4	48	6	AX426920	AX426920 Sequence
27	22.2	1.4	28	6	AX203828	AX203828 Sequence
28	22	1.3	22	6	AR130451	AR130451 Sequence
29	22	1.3	22	6	E09226	E09226 Primer for
c 30	22	1.3	22	6	E09227	E09227 Primer for
31	22	1.3	48	6	I33522	I33522 Sequence 1
c 32	22	1.3	50	8	CNS018YM	AL110965 Botrytis
c 33	21.8	1.3	47	6	AX114372	AX114372 Sequence
c 34	21.8	1.3	48	6	I33523	I33523 Sequence 2
35	21.6	1.3	41	6	AR164944	AR164944 Sequence
36	21.6	1.3	41	6	E22883	E22883 DNA sequenc
c 37	21.6	1.3	50	6	AX160081	AX160081 Sequence
c 38	21.6	1.3	50	6	AX160578	AX160578 Sequence
c 39	21.4	1.3	43	6	AX484483	AX484483 Sequence
c 40	21.4	1.3	47	1	LACDRRH	M84772 Lactococcus
c 41	21.4	1.3	48	9	S64862S2	S64863 alpha 1-the
c 42	21.2	1.3	43	6	AX484516	AX484516 Sequence
c 43	21.2	1.3	45	8	AB008098	AB008098 Saccharom
44	21.2	1.3	50	6	AX157057	AX157057 Sequence
45	21	1.3	21	6	A56957	A56957 Sequence 15

ALIGNMENTS

RESULT 1
AR021184
LOCUS AR021184 47 bp DNA linear PAT 05-DEC-1998
DEFINITION Sequence 42 from patent US 5789539.
ACCESSION AR021184
VERSION AR021184.1 GI:3975799
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 47)
AUTHORS Daly,T.J. and LaRosa,G.J.
TITLE Chemokine-like proteins and methods of use
JOURNAL Patent: US 5789539-A 42 04-AUG-1998;
FEATURES Location/Qualifiers

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     source          1. .47
                     /organism="unknown"
BASE COUNT       17 a     10 c     10 g     10 t
ORIGIN

  Query Match             2.3%;  Score 37.4;  DB 6;  Length 47;
  Best Local Similarity   87.2%;  Pred. No. 2.8e+04;
  Matches   41;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy     169 AGGAGTGCTAAAGAACTTAGATGTCAGTGCATAAAGACATACTCCAA 215
           | ||||||||||| ||    |||||||||||||||||||||||||
Db       1 ATGAGTGCTAAAGACCTGCAGTGTCAGTGCATAAAGACATACTCCAA 47


RESULT 2
I60565
LOCUS       I60565                    47 bp    DNA     linear   PAT 07-OCT-1997
DEFINITION  Sequence 42 from patent US 5656724.
ACCESSION   I60565
VERSION     I60565.1  GI:2479010
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 47)
  AUTHORS   Daly,T.J. and LaRosa,G.J.
  TITLE     Chemokine-like proteins and methods of use
  JOURNAL   Patent: US 5656724-A 42 12-AUG-1997;
FEATURES             Location/Qualifiers
     source          1. .47
                     /organism="unknown"
BASE COUNT       17 a     10 c     10 g     10 t
ORIGIN

  Query Match             2.3%;  Score 37.4;  DB 6;  Length 47;
  Best Local Similarity   87.2%;  Pred. No. 2.8e+04;
  Matches   41;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy     169 AGGAGTGCTAAAGAACTTAGATGTCAGTGCATAAAGACATACTCCAA 215
           | ||||||||||| ||    |||||||||||||||||||||||||
Db       1 ATGAGTGCTAAAGACCTGCAGTGTCAGTGCATAAAGACATACTCCAA 47


RESULT 3
AR021182/c
LOCUS       AR021182                  37 bp    DNA     linear   PAT 05-DEC-1998
DEFINITION  Sequence 40 from patent US 5789539.
ACCESSION   AR021182
VERSION     AR021182.1  GI:3975797
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 37)
  AUTHORS   Daly,T.J. and LaRosa,G.J.
  TITLE     Chemokine-like proteins and methods of use
  JOURNAL   Patent: US 5789539-A 40 04-AUG-1998;
FEATURES             Location/Qualifiers
     source          1. .37
                     /organism="unknown"
BASE COUNT       11 a     14 c      2 g     10 t
ORIGIN

  Query Match             2.3%;  Score 37;  DB 6;  Length 37;
  Best Local Similarity   100.0%;  Pred. No. 3.4e+04;
  Matches   37;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     351 GGTTGTGGAGAAGTTTTTGAAGAGGGCTGAGAATTCA 387
           |||||||||||||||||||||||||||||||||||||
Db      37 GGTTGTGGAGAAGTTTTTGAAGAGGGCTGAGAATTCA 1


RESULT 4
```

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I60563/c
LOCUS       I60563                    37 bp    DNA     linear   PAT 07-OCT-1997
DEFINITION  Sequence 40 from patent US 5656724.
ACCESSION   I60563
VERSION     I60563.1  GI:2479008
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 37)
  AUTHORS   Daly,T.J. and LaRosa,G.J.
  TITLE     Chemokine-like proteins and methods of use
  JOURNAL   Patent: US 5656724-A 40 12-AUG-1997;
FEATURES             Location/Qualifiers
     source          1. .37
                     /organism="unknown"
BASE COUNT       11 a     14 c      2 g     10 t
ORIGIN

  Query Match             2.3%;  Score 37;  DB 6;  Length 37;
  Best Local Similarity   100.0%;  Pred. No. 3.4e+04;
  Matches   37;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     351 GGTTGTGGAGAAGTTTTTGAAGAGGGCTGAGAATTCA 387
           |||||||||||||||||||||||||||||||||||||
Db      37 GGTTGTGGAGAAGTTTTTGAAGAGGGCTGAGAATTCA 1


RESULT 5
A56958/c
LOCUS       A56958                    33 bp    DNA     linear   PAT 03-MAR-1998
DEFINITION  Sequence 16 from Patent WO9629091.
ACCESSION   A56958
VERSION     A56958.1  GI:3712941
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 33)
  AUTHORS   Stanley,M.A. and Scarpini,C.G.
  TITLE     TREATMENT OF PAPILLOMAVIRUS-ASSOCIATED LESIONS USING INTERLEUKIN-12
  JOURNAL   Patent: WO 9629091-A 16 26-SEP-1996;
            UNIV CAMBRIDGE TECH (GB)
COMMENT     Other publication AU 5151596 961008.
FEATURES             Location/Qualifiers
     source          1. .33
                     /organism="unidentified"
                     /db_xref="taxon:32644"
BASE COUNT        9 a     10 c      2 g     12 t
ORIGIN

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  Best Local Similarity   100.0%;  Pred. No. 1.4e+05;
  Matches   33;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     358 GAGAAGTTTTTGAAGAGGGCTGAGAATTCATAA 390
           |||||||||||||||||||||||||||||||||
Db      33 GAGAAGTTTTTGAAGAGGGCTGAGAATTCATAA 1


RESULT 6
AR052918/c
LOCUS       AR052918                  33 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 42 from patent US 5833976.
ACCESSION   AR052918
VERSION     AR052918.1  GI:5977780
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 33)
  AUTHORS   Malefyt,Rde.Waal., Howard,M., Hsu,D.-H., Ishida,H., O'Garra,A.,
            Spits,H. and Zlotnik,A.
```

```
  TITLE     Use of interleukin-10 (IL-10) to treat endotoxin- or
            superantigen-induced toxicity
  JOURNAL   Patent: US 5833976-A 42 10-NOV-1998;
FEATURES             Location/Qualifiers
     source          1. .33
                     /organism="unknown"
BASE COUNT        9 a      10 c       2 g      12 t
ORIGIN

  Query Match             2.0%;  Score 33;  DB 6;  Length 33;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+05;
  Matches   33;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    358 GAGAAGTTTTTGAAGAGGGCTGAGAATTCATAA 390
          |||||||||||||||||||||||||||||||||
Db     33 GAGAAGTTTTTGAAGAGGGCTGAGAATTCATAA 1


RESULT 7
AR054281/c
LOCUS       AR054281                  33 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 42 from patent US 5837232.
ACCESSION   AR054281
VERSION     AR054281.1  GI:5979858
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 33)
  AUTHORS   De Waal Malefyt,R., Howard,M., Hsu,D.-H., Ishida,H., O'Garra,A.,
            Spits,H. and Zlotnik,A.
  TITLE     Use of an interleukin-10 antagonist to treat a B cell mediated
            autoimmune disorder
  JOURNAL   Patent: US 5837232-A 42 17-NOV-1998;
FEATURES             Location/Qualifiers
     source          1. .33
                     /organism="unknown"
BASE COUNT        9 a      10 c       2 g      12 t
ORIGIN

  Query Match             2.0%;  Score 33;  DB 6;  Length 33;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+05;
  Matches   33;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    358 GAGAAGTTTTTGAAGAGGGCTGAGAATTCATAA 390
          |||||||||||||||||||||||||||||||||
Db     33 GAGAAGTTTTTGAAGAGGGCTGAGAATTCATAA 1


RESULT 8
AR054483/c
LOCUS       AR054483                  33 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 42 from patent US 5837293.
ACCESSION   AR054483
VERSION     AR054483.1  GI:5980060
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 33)
  AUTHORS   De Waal Malefyt,R., Howard,M., Hsu,D.-H., Ishida,H., O'Garra,A.,
            Spits,H. and Zlotnik,A.
  TITLE     Use of interleukin-10 analogs for antagonists to treat endotoxin-
            or superantigen-induced toxicity
  JOURNAL   Patent: US 5837293-A 42 17-NOV-1998;
FEATURES             Location/Qualifiers
     source          1. .33
                     /organism="unknown"
BASE COUNT        9 a      10 c       2 g      12 t
ORIGIN

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  Best Local Similarity   100.0%;  Pred. No. 1.4e+05;
  Matches   33;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    358 GAGAAGTTTTTGAAGAGGGCTGAGAATTCATAA 390
          |||||||||||||||||||||||||||||||||
Db     33 GAGAAGTTTTTGAAGAGGGCTGAGAATTCATAA 1


RESULT 9
AX249279
LOCUS       AX249279                  31 bp    DNA     linear   PAT 28-SEP-2001
DEFINITION  Sequence 1358 from Patent WO0166800.
ACCESSION   AX249279
VERSION     AX249279.1  GI:15863902
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 31)
  AUTHORS   Cargill,M., Ireland,J.S. and Lander,E.S.
  TITLE     Human single nucleotide polymorphisms
  JOURNAL   Patent: WO 0166800-A 1358 13-SEP-2001;
            WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US)
FEATURES             Location/Qualifiers
     source          1. .31
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
BASE COUNT       11 a       8 c       4 g       7 t       1 others
ORIGIN

  Query Match             1.9%;  Score 30.6;  DB 6;  Length 31;
  Best Local Similarity   96.8%;  Pred. No. 3.4e+05;
  Matches   30;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    220 TTCCACCCCAAATTTATCAAAGAACTGAGAG 250
          |||||||||||||||:|||||||||||||||
Db      1 TTCCACCCCAAATTTMTCAAAGAACTGAGAG 31


RESULT 10
AR200024/c
LOCUS       AR200024                  30 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 6 from patent US 6355775.
ACCESSION   AR200024
VERSION     AR200024.1  GI:20250098
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Nagasawa,Y. and Yoshida,H.
  TITLE     Transcriptional inhibitor
  JOURNAL   Patent: US 6355775-A 6 12-MAR-2002;
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="unknown"
BASE COUNT        3 a       7 c       8 g      12 t
ORIGIN

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  Best Local Similarity   100.0%;  Pred. No. 4.3e+05;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     14 GACAGCAGAGCACACAAGCTTCTAGGACAA 43
          ||||||||||||||||||||||||||||||
Db     30 GACAGCAGAGCACACAAGCTTCTAGGACAA 1


RESULT 11
AX419968/c
LOCUS       AX419968                  30 bp    DNA     linear   PAT 18-JUN-2002
DEFINITION  Sequence 305 from Patent WO0198537.
ACCESSION   AX419968
```

```
VERSION     AX419968.1  GI:21524335
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Lyamichev,V., Allawi,H., Dong,F., Neri,B.P. and Vener,I.T.
  TITLE     Nucleic acid accessible hybridization sites
  JOURNAL   Patent: WO 0198537-A 305 27-DEC-2001;
            THIRD WAVE TECHNOLOGIES, INC. (US)
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
BASE COUNT       13 a      4 c      2 g     11 t
ORIGIN

  Query Match             1.8%;  Score 30;  DB 6;  Length 30;
  Best Local Similarity   100.0%;  Pred. No. 4.3e+05;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    1165 ATGATGTTTTATTAGATAAATTTCAATCAG 1194
           ||||||||||||||||||||||||||||||
Db      30 ATGATGTTTTATTAGATAAATTTCAATCAG 1


RESULT 12
BD004257/c
LOCUS       BD004257                  30 bp    DNA     linear   PAT 31-JAN-2002
DEFINITION  Method for searching physiologically active substance.
ACCESSION   BD004257
VERSION     BD004257.1  GI:18632218
KEYWORDS    JP 2001037492-A/3.
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Koishi,R., Yoshimura,C. and Serizawa,N.
  TITLE     Method for searching physiologically active substance
  JOURNAL   Patent: JP 2001037492-A 3 13-FEB-2001;
            SANKYO CO LTD
COMMENT     OS   Artificial Sequence
            PN   JP 2001037492-A/3
            PD   13-FEB-2001
            PF   24-MAY-2000 JP 2000152282
            PR
            PI   RYUTA KOISHI,CHIGUSA YOSHIMURA,NOBUKI SERIZAWA PC
            C12N15/09,C12N5/10,C12Q1/02,C12N15/00,C12N5/00 CC
            FH   Key             Location/Qualifiers
            FT   source          1. .30
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
BASE COUNT        3 a      7 c      8 g     12 t
ORIGIN

  Query Match             1.8%;  Score 30;  DB 6;  Length 30;
  Best Local Similarity   100.0%;  Pred. No. 4.3e+05;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      14 GACAGCAGAGCACACAAGCTTCTAGGACAA 43
           ||||||||||||||||||||||||||||||
Db      30 GACAGCAGAGCACACAAGCTTCTAGGACAA 1


RESULT 13
AX317616/c
LOCUS       AX317616                  29 bp    DNA     linear   PAT 14-DEC-2001
DEFINITION  Sequence 619 from Patent WO0190337.
ACCESSION   AX317616
VERSION     AX317616.1  GI:17900517
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Allawi,H., Bartholomay,C.T., Chehak,L., Curtis,M.L., Eis,P.S.,
            Hall,J.G., Ip,H.S., Kaiser,M., Kwiatkowski,R.W., Lukowiak,A.A.,
            Lyamichev,V., Ma,W., Olson-Munoz,M.C., Olson,S.M., Schaefer,J.J.,
            Skrzypczynski,Z., Takova,T.Y., Vedvik,K.L. and Lyamichev,N.E.
  TITLE     Detection of rna
  JOURNAL   Patent: WO 0190337-A 619 29-NOV-2001;
            THIRD WAVE TECHNOLOGIES, INC. (US)
FEATURES             Location/Qualifiers
     source          1. .29
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
BASE COUNT        8 a      0 c     11 g     10 t
ORIGIN

  Query Match             1.8%;  Score 29;  DB 6;  Length 29;
  Best Local Similarity   100.0%;  Pred. No. 6.2e+05;
  Matches   29;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     211 TCCAAACCTTTCCACCCCAAATTTATCAA 239
           |||||||||||||||||||||||||||||
Db      29 TCCAAACCTTTCCACCCCAAATTTATCAA 1


RESULT 14
AR090359
LOCUS       AR090359                  28 bp    DNA     linear   PAT 07-SEP-2000
DEFINITION  Sequence 479 from patent US 5994076.
ACCESSION   AR090359
VERSION     AR090359.1  GI:10017114
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 28)
  AUTHORS   Chenchik,A., Jokhadze,G. and Bibilashvilli,R.
  TITLE     Methods of assaying differential expression
  JOURNAL   Patent: US 5994076-A 479 30-NOV-1999;
FEATURES             Location/Qualifiers
     source          1. .28
                     /organism="unknown"
BASE COUNT        6 a      9 c      7 g      6 t
ORIGIN

  Query Match             1.7%;  Score 28;  DB 6;  Length 28;
  Best Local Similarity   100.0%;  Pred. No. 8.8e+05;
  Matches   28;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      88 AACATGACTTCCAAGCTGGCCGTGGCTC 115
           ||||||||||||||||||||||||||||
Db       1 AACATGACTTCCAAGCTGGCCGTGGCTC 28


RESULT 15
AR090360/c
LOCUS       AR090360                  28 bp    DNA     linear   PAT 07-SEP-2000
DEFINITION  Sequence 480 from patent US 5994076.
ACCESSION   AR090360
VERSION     AR090360.1  GI:10017115
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 28)
  AUTHORS   Chenchik,A., Jokhadze,G. and Bibilashvilli,R.
  TITLE     Methods of assaying differential expression
  JOURNAL   Patent: US 5994076-A 480 30-NOV-1999;
FEATURES             Location/Qualifiers
     source          1. .28
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                     /organism="unknown"
BASE COUNT        5 a      10 c       6 g       7 t
ORIGIN

  Query Match             1.7%;  Score 28;  DB 6;  Length 28;
  Best Local Similarity   100.0%;  Pred. No. 8.8e+05;
  Matches   28;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    248 GAGTGATTGAGAGTGGACCACACTGCGC 275
          ||||||||||||||||||||||||||||
Db     28 GAGTGATTGAGAGTGGACCACACTGCGC 1


RESULT 16
AR197394
LOCUS       AR197394                 28 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 479 from patent US 6352829.
ACCESSION   AR197394
VERSION     AR197394.1  GI:20247243
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 28)
  AUTHORS   Chenchik,A., Jokhadze,G. and Bibilashvilli,R.
  TITLE     Methods of assaying differential expression
  JOURNAL   Patent: US 6352829-A 479 05-MAR-2002;
FEATURES             Location/Qualifiers
     source          1. .28
                     /organism="unknown"
BASE COUNT        6 a      9 c       7 g       6 t
ORIGIN

  Query Match             1.7%;  Score 28;  DB 6;  Length 28;
  Best Local Similarity   100.0%;  Pred. No. 8.8e+05;
  Matches   28;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     88 AACATGACTTCCAAGCTGGCCGTGGCTC 115
          ||||||||||||||||||||||||||||
Db      1 AACATGACTTCCAAGCTGGCCGTGGCTC 28


RESULT 17
AR197395/c
LOCUS       AR197395                 28 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 480 from patent US 6352829.
ACCESSION   AR197395
VERSION     AR197395.1  GI:20247244
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 28)
  AUTHORS   Chenchik,A., Jokhadze,G. and Bibilashvilli,R.
  TITLE     Methods of assaying differential expression
  JOURNAL   Patent: US 6352829-A 480 05-MAR-2002;
FEATURES             Location/Qualifiers
     source          1. .28
                     /organism="unknown"
BASE COUNT        5 a      10 c       6 g       7 t
ORIGIN

  Query Match             1.7%;  Score 28;  DB 6;  Length 28;
  Best Local Similarity   100.0%;  Pred. No. 8.8e+05;
  Matches   28;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    248 GAGTGATTGAGAGTGGACCACACTGCGC 275
          ||||||||||||||||||||||||||||
Db     28 GAGTGATTGAGAGTGGACCACACTGCGC 1


RESULT 18
AX280042
LOCUS       AX280042                 26 bp    DNA     linear   PAT 02-NOV-2001
DEFINITION  Sequence 17 from Patent WO0177382.
ACCESSION   AX280042
VERSION     AX280042.1  GI:16607493
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Hull,J. and Kwiatkowski,D.P.
  TITLE     Genetic factor affecting cytokine expression
  JOURNAL   Patent: WO 0177382-A 17 18-OCT-2001;
            ISIS INNOVATION LIMITED (GB)
FEATURES             Location/Qualifiers
     source          1. .26
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="Oligonucleotide"
BASE COUNT        9 a      5 c       2 g      10 t
ORIGIN

  Query Match             1.6%;  Score 26;  DB 6;  Length 26;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+06;
  Matches   26;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   1228 CCCAGTTAAATTTTCATTTCAGATAA 1253
          ||||||||||||||||||||||||||
Db      1 CCCAGTTAAATTTTCATTTCAGATAA 26


RESULT 19
I22270/c
LOCUS       I22270                   25 bp    DNA     linear   PAT 07-OCT-1996
DEFINITION  Sequence 8 from patent US 5527678.
ACCESSION   I22270
VERSION     I22270.1  GI:1602624
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   Blaser,M.J., Tummuru,M.K.R. and Sharma,S.A.
  TITLE     CagB and CagC genes of helicobacter pylori and related compositions
  JOURNAL   Patent: US 5527678-A 8 18-JUN-1996;
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="unknown"
BASE COUNT        6 a      10 c       1 g       8 t
ORIGIN

  Query Match             1.5%;  Score 25;  DB 6;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 2.6e+06;
  Matches   25;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    358 GAGAAGTTTTTGAAGAGGGCTGAGA 382
          |||||||||||||||||||||||||
Db     25 GAGAAGTTTTTGAAGAGGGCTGAGA 1


RESULT 20
AX280041
LOCUS       AX280041                 26 bp    DNA     linear   PAT 02-NOV-2001
DEFINITION  Sequence 16 from Patent WO0177382.
ACCESSION   AX280041
VERSION     AX280041.1  GI:16607492
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Hull,J. and Kwiatkowski,D.P.
  TITLE     Genetic factor affecting cytokine expression
  JOURNAL   Patent: WO 0177382-A 16 18-OCT-2001;
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ISIS INNOVATION LIMITED (GB)

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FEATURES             Location/Qualifiers
     source          1. .26
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="Oligonucleotide"
BASE COUNT        8 a      5 c      2 g     11 t
ORIGIN

  Query Match             1.5%;  Score 25;  DB 6;  Length 26;
  Best Local Similarity   100.0%;  Pred. No. 2.6e+06;
  Matches   25;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   1228 CCCAGTTAAATTTTCATTTCAGATA 1252
           |||||||||||||||||||||||||
Db      1 CCCAGTTAAATTTTCATTTCAGATA 25


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